MONOGRAM
CEREALS & GRASSES RESEARCH NETWORK

MonoGram 2023
network meeting

3–5 April 2023

University of Reading

HOSTED BY
University of Reading
School of Agriculture,
Policy and Development
Whiteknights Campus

BOOKLET SPONSORED BY
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WELCOME

The University of Reading in its modern form was established by royal charter in 1926 though it traces its origins back to the foundation in 1892 as University College, Reading, a University of Oxford extension college. Its main Whiteknights campus has won the prestigious Green Flag award on multiple occasions.

In its early days, Professor John Percival and colleagues were the driving force in the founding of the discipline of Agricultural Botany, while today Reading is the leading UK University in the 2022 QS World University rankings for Agriculture and Forestry and boasts excellent facilities supporting its world-class agricultural research mission.

Whiteknights campus hosts the Crop and Environment Laboratory, a state-of-the-art controlled environment facility dedicated to crop physiology and crop breeding research. The University of Reading's Crop Research Unit (CRU) is located within the 180 ha Sonning farm, occupying approximately 15 ha of the University's most uniform soil and undertakes research on all aspects of arable, soft fruit and forage crop production. The University's 500 ha Arborfield Farm hosts the Centre for Dairy Research (CEDAR), a unique facility for applied and strategic large animal research, addressing key issues for the sustainability of animal production systems and animal behaviour and welfare.

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Day 1 Monday 3 April

09:30–11:00	**Registration in the Palmer Building foyer** (Building 26 on campus map, p10)
11:00–11:15	**Welcome** Paola Tosi (University of Reading)
11:15	**Keynote Speaker:** Professor Frank Ordon (Julius Kuehn Institute, Germany) **Breeding for resistance – key to solving future challenges in cereal production**
12:30–13:30	**Lunch**
13:30–15:00	**SESSION I: Interactions with pathogenic and beneficial organisms** Chairs: Carmen Escudero-Martinez and Alexey Mikaberidze
13:30–14:00	**How to manage the major wheat disease septoria tritici blotch caused by remarkably large and diverse pathogen populations** Alexey Mikaberidze (University of Reading)
14:00	**Allele-specific immunity in barley to divergent cereal rusts conferred by immune receptors with different integrated domains** Li Long (The Sainsbury Laboratory)
14:20	**Wheat RILs differing in yield, root architecture and mucilage secretion show associated changes in rhizosheath microbiome composition** Eric Ober (NIAB)
14:40	**Genome-wide association study to map genes linked with take-all resistance in wheat using the Watkins landraces** Nida Ghori (Rothamsted Research)
15:00–15:30	**Coffee**
15:30–17:00	**SESSION II: End use quality and nutrition** Co-chairs: Paola Tosi (University of Reading) and Peter Shewry (Rothamsted Research)
15:30	**Do NAC transcription factors regulate the timing of leaf senescence and wheat grain protein content?** Catherine E B Evans (John Innes Centre)
15:45	**Distinct biochemical mechanisms are involved in the initiation of A- and B-type starch granules during wheat grain development** Nitin Uttam Kamble (John Innes Centre)
16:00	**Multiplexed genome editing reduces polyphenol oxidase activity in wheat grains** Stephen Pearce (Rothamsted Research)
16:15	**Unravelling the biochemical and genetic basis of the perfect cookie making wheat** Peter Abu Jabir (University of Reading)
16:30	**Iron-rich wheat: a solution for anaemia in developing countries** Muhammad Ali (John Innes Centre)
17:00	Poster flash (18 x two-minute presentations)
17:45	Poster session (sponsored by SEB centenary celebration)

Day 2 Tuesday 4 April

08:00	Women in Cereal Science Coffee
09:00–10:30	**SESSION III: Physiology and resource use** Chairs: Joshua Ham (RATG) and Julie King (University of Nottingham)
9:00	**Photosynthetic heat tolerance in wheat's wild relatives** Stella Edwards (University of Nottingham)
9:30	**Chlorophyll fluorescence-based phenotyping for dissecting the genetic basis of cereal-environment interactions** John Ferguson (University of Essex)
9:50	**Assessing Irish heritage barley in response to waterlogging: an image-based phenotyping approach** Patrick Langan (University College Dublin)
10:10	**Addressing the challenge of combined drought and heat stress for wheat production** Arisede Chisaka (University of Reading)
10:30–11:00	**Coffee** (Sponsored by Limagrain)
11:00–12:30	**SESSION IV: Developmental processes** Chairs: Laura Dixon (University of Leeds) and Adam Gauley (AFBI)
11:00	**A grass specific gene regulating recombination in barley** Jamie Orr (James Hutton Institute)
11:15	**VRNturing into the unknown: dissecting the role of *VRN2* in climate adaptation** Dominique Hirsz (University of Leeds)
11:30	**Source-sink strength determines grain yield in the spike branching 'Miracle-Wheat'** Ragavendran Abbai (IPK Gatersleben)
11:45	**Genetic control of awn roughness in barley** Muhammad Awais (IPK Gatersleben)
12:00	**Crazy leaves and truffula trees: Unravelling auxin signalling underpinning maize architecture** Annis Richardson (University of Edinburgh)
12:30–13:30	**Lunch**
13:30–15:00	**SESSION V: Bioinformatics and genomics** Chairs: Philippa Borrill (John Innes Centre) and Rachel Goddard (Limagrain)
13:30	**Genomic resources for a historical collection of cultivated two-row European spring barley genotypes** Miriam Schreiber (James Hutton Institute)
13:45	**Ensembl Plants and the PanOryza Project** Shradha Saraf (European Bioinformatics Institute)
14:00	**Using EMS mutagenesis to find the gametocidal gene in a wheat-*Aegilops sharonensis* introgression line** Nicola Walter (University of Nottingham)

14:15	**Breaking the bottleneck: exploring quantitative genetics to unlock the potential of synthetic hexaploid wheat** Tally Wright (NIAB)
14:30	**Double trouble – assembling the complex allelic diversity in outcrossed tetraploid Urochloa decumbens grass** Camilla Ryan (Earlham Institute)
15:00–15:30	**Coffee**
15:30–16:40	**MECEA winners talks**
15:30	**MECEA winner PhD**
16:00	**MECEA winner Post-doctoral**
16:40–18:30	Poster session
20:00	**Workshop dinner** Meadow Suite, Park House (Building 8 on campus map, p10)

Day 3 Wednesday 5 April

09:15–09:25	**Introduction to the Rank Prize** Professor Malcolm Bennett (Rank Prize Nutrition Committee)
09:25–10:15	**Rank Prize ECR excellence lecture** **Manipulating photosynthesis to boost crop productivity in a warming world** Amanda P Cavanagh (University of Essex)
10:15–11:00	**Rank lecture** **Coordinating research to support sustainable wheat production** Simon Griffiths (John Innes Centre)
11:00–11:30	**Coffee**
11:30–13:00	**SESSION VI: Sustainable systems** Co-chairs: Stephanie Swarbreck (NIAB) and Aiswarya Girija (Aberystwyth University)
11:30	**Rising with the flow: maximizing plant resilience by exploring the connection between vascular structure and water use efficiency in cereal crops** Pallavi Singh (University of Essex)
12:00	**Gravitropism & steeper, deeper rooting in wheat root systems** Fay Walsh (University of Leeds)
12:20	**Identifying master-regulators of abiotic stress responses in bread wheat using a network approach** Liam Barrett (University of York)
12:40	**From images to loci: embedding AI in smartphones and drones to enable field-based yield phenotyping and mapping genetics underlying key yield components in wheat** Ji Zhou (NIAB)
13:00	Announcement about Monogram 2024 **End of conference**
13:15–14:15	**Lunch**
14:15–15:00	Tour of University of Reading glasshouse and control environment facilities (optional)

KEYNOTE SPEAKERS

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Professor Frank Ordon

Julius Kühn-Institute (JKI), Germany

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www.julius-kuehn.de/en/structure/president/

Frank Ordon is President of the Julius Kühn-Institute (JKI), Federal Research Centre for Cultivated Plants in Germany – a research institution and a higher federal authority affiliated with the German Federal Ministry of Food and Agriculture. He is honorary professor for 'Molecular Resistance Breeding' at the Martin-Luther-University, Halle-Wittenberg, Germany. His research interest is the estimation of genetic diversity in several crop species and its exploitation by genomic tools, e.g. the development of molecular markers for resistance genes to fungal and viral pathogens up to gene isolation. He published his results in about 180 peer reviewed papers.

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Dr Amanda Cavanagh

School of Life Sciences, University of Essex

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@cavycavs @PlantEssex

Dr. Amanda Cavanagh is a lecturer at the University of Essex. Her research interest in plant environmental physiology covers molecular biology, biochemistry, and leaf physiology. Amanda completed her PhD at the University of New Brunswick in Canada, where she worked on Rubisco – the enzyme that feeds the world. During her postdoc at the University of Illinois at Urbana-Champaign in the USA, she tested synthetic biology pathways that improve photosynthetic performance in crops under field and environmental stress conditions.

At the University of Essex, her lab explores leaf and enzyme-level responses of photosynthesis, and is developing strategies to optimize crop performance in response to the changing climate.

Dr Simon Griffiths

The John Innes Centre,
Norwich Research Park, Norwich

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www.jic.ac.uk/people/simon-griffiths/

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RANK PRIZE

Dr Simon Griffiths is the programme leader of BBSRC ‘Designing Future Wheat’ (DFW) programme (designingfuturewheat.org.uk/) and also of the new programme ‘Delivering Sustainable Wheat’ (DSW), which began this month (April 2023).

He Chairs the DFW/DSW Breeders Toolkit Committee (**designingfuturewheat.org.uk/breeders-toolkit/**) which tries to translate scientific discoveries into breeding impact. His team contributes to the BTK by finding new and useful genetic variation in the AE Watkins landrace collection.

The identification of genes controlling the timing of phenology phases and crop height are a major focus of the research in his team, but they are also interested in supporting groups working on human nutritional traits via their expertise in genetics and genomics of wheat.

Monogram committee members

Philippa Borrill
(John Innes Centre)

Paola Tosi
(University of Reading)

Laura Dixon
(University of Leeds)

Carmen Escudero-Martinez
(University of Dundee)

Rachel Goddard
(Limagrain)

Surbhi Grewal
(University of Nottingham)

Joshua Ham
(RAGT)

Carus John-Bejai
(KWS)

Tim Langdon
(University of Aberystwyth)

Alison Lovegrove
(Rothamsted Research)

Paul Nicholson
(John Innes Centre)

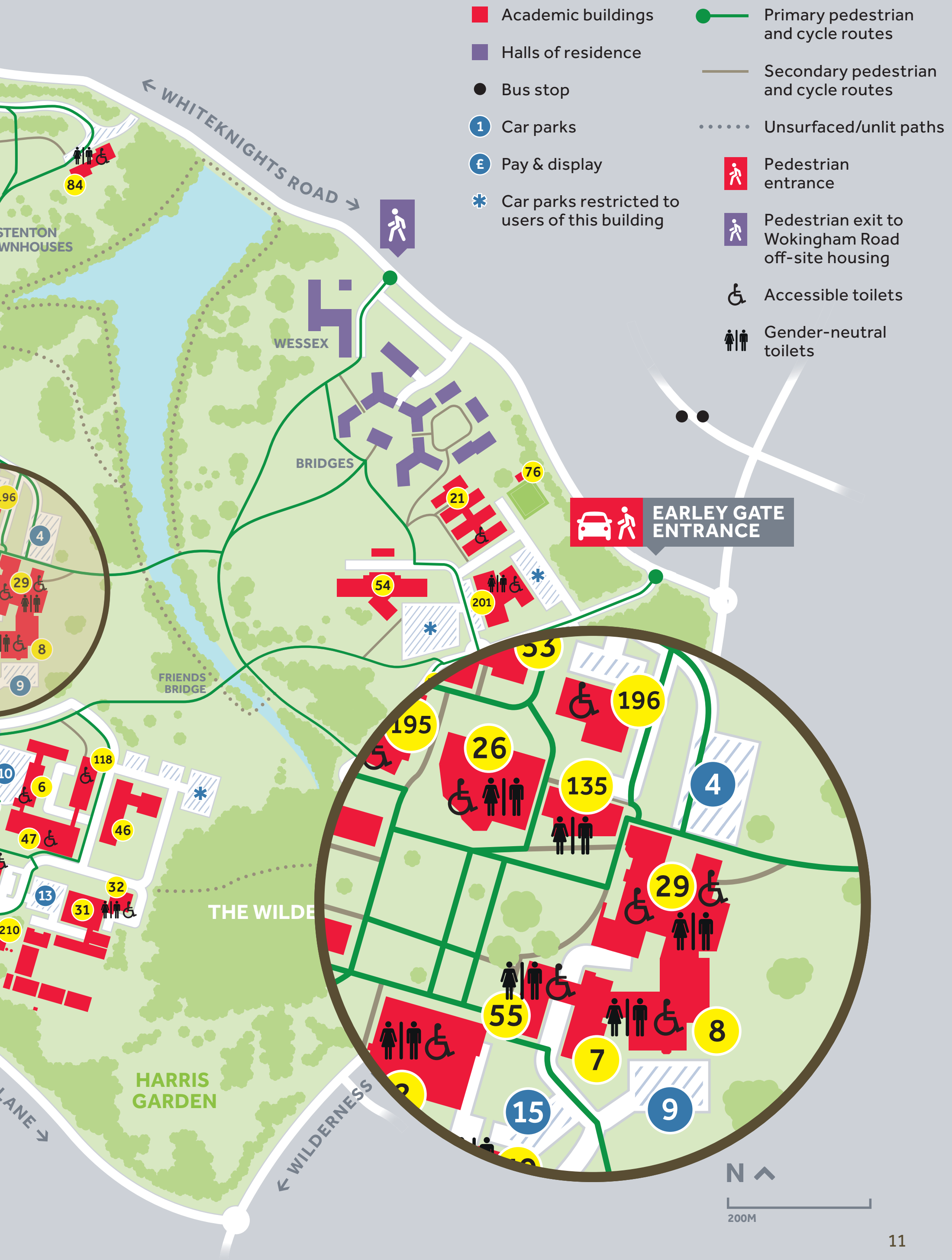
Miriam Schreiber
(James Hutton Institute)

Stéphanie Swarbreck
(NIAB)

WHITEKNIGHTS CAMPUS

Monogram event: Palmer Building 26

If coming by car use Shinfield Road entrance (RG6 6UR) and Car Park 1a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ABSTRACTS

KEYNOTE SPEAKER

Professor Frank Ordon, Julius Kuehn Institute

Breeding for resistance – key to solving future challenges in cereal production

In 2050 about ten billion people have to be fed in the background of climate change, the loss of biodiversity and crisis – actually the Ukrainian war. In addition, the EU Farm to Fork Strategy recommends a reduction of the use, respectively risk, of pesticides by 50% up to 2030 and an increase of the acreage of eco farming to 25%. Furthermore, new pathogens are gaining rising importance due to climate change. In this respect, breeding for resistance is of prime importance to meet future challenges in cereal production.

Resistance breeding has been quite successful in the last decades already, e.g. demonstrated by improving resistance simultaneously to yield in German winter wheat cultivars. This success has been mainly due to traditional selection schemes complemented by doubled haploid technologies and marker based selection procedures.

Today, high throughput marker systems and knowledge of the genome sequence of cereals on the one hand facilitate new selection strategies, but also facilitate a more targeted use of genetic resources, which are a treasure trove for improving resistance. Respective techniques facilitate the efficient development of markers for major genes and quantitative trait loci (QTL) by genome wide association studies and pave the way for an enhanced gene isolation. Knowledge of these genes transfers breeding to the allele level and facilitates the sequenced based identification of novel alleles in large gene bank collections and their directed use in plant breeding as well as the creation of new alleles by genome editing. Furthermore, priming and optimizing the respective genetic interaction may be an option for enhancing resistance in cereals. Examples of using these genomic tools to improve resistance to fungal and viral pathogens as well as to insects are presented.

Alexey Mikaberidze, University of Reading

How to manage the major wheat disease septoria tritici blotch caused by remarkably large and diverse pathogen populations?

Populations of plant pathogens carrying higher genetic diversity are thought to have a greater evolutionary potential than populations carrying less diversity. We estimated the ranges of values associated with two components of genetic diversity, the number of unique pathogen genotypes and the number of spores produced during an epidemic, for the septoria tritici blotch (STB) pathogen *Zymoseptoria tritici*. We found that wheat fields experiencing typical levels of infection are likely to carry between 3.2 and 14.9 million pathogen genotypes per hectare produce 2.3 to 10.5 trillion pycnidiospores per hectare. Among these, 28 to 130 million pathogen spores carry adaptive mutations to counteract fungicides/resistant cultivars[1]. These findings suggest a need to re-evaluate strategies to manage STB in a more sustainable manner. Using STB-tolerant wheat cultivars[2] and cultivar mixtures[3] are promising components of such strategies, because these measures minimize selection exerted on pathogen populations.

[1] https://doi.org/10.1101/2022.03.13.484150
[2] https://doi.org/10.1111/nph.16418
[3] https://doi.org/10.1111/ppa.13247

Li Long, The Sainsbury Laboratory

Allele-specific immunity in barley to divergent cereal rusts conferred by immune receptors with different integrated domains

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Li Long, Inmaculada Hernandez-Pinzon, Phon Green,
Brian Steffenson, Yunfeng Jiang, Guoyue Chen,
Matthew James Moscou

Stripe rust caused by *Puccinia striiformis* f. sp. *tritici* (*Pst*) is a major threat to wheat worldwide production. *Pst* exhibits host species specificity with different lineages adapted to different grass species. In previous work, we found that non-adapted resistance in domesticated barley to wheat stripe rust was primarily conferred by three resistance genes, *Rps6*, *Rps7*, and *Rps8*. In this study, WBDC266 carries a new resistance gene to wheat stripe rust, *Rps10*, which is located on chromosome 5HL. Haplotype variation in the NLR encoding genes *Rga1* and *Rpg5* were predictive of the presence or absence of *Rps10*. Our results show that the allele of *Rpg5* in WBDC266 encodes an integrated NLR with a domain derived from a CBP60 and protein kinase domain derived from the DLSV family. Collectively, this work has links allelic variation in immunity to divergent cereal rusts and implicates two lineage-specific subfamilies in grass immunity.

Eric Ober, NIAB

Wheat RILs differing in yield, root architecture and mucilage secretion show associated changes in rhizosheath microbiome composition

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Emily Marr, Greg Deakin, Eric Ober

Microbial activity in the rhizosphere influences plant processes including nutrient and water uptake, and in turn roots can affect the microbiome. We tested the hypothesis that wheat lines differing in root system architecture (RSA) and yield potential would harbour differences in the composition of the associated soil microbiome. A 16S and ITS metagenomics analysis was conducted on samples of seedling rhizosheath soil from 25 doubled haploid RILs of the Avalon x Cadenza mapping population. Higher-yielding lines differed significantly from lower-yielding lines for fungal but not bacterial species composition. Genotypic differences in seminal root angle and amounts of several secreted root polysaccharides were associated with differences in bacterial and fungal species composition and various diversity indices. Combining metagenomics data with genetic control of RSA and mucilage composition provides a picture of rhizosphere dynamics, with the potential to engineer the rhizosphere environment to benefit crop sustainability.

Nida Ghori, Rothamsted Research

Genome-wide association study to map genes linked with take-all resistance in wheat using the Watkins landraces

Nida Ghori, Gail Canning, Luzie Wingen, Dan Smith, Jitender Chaama and Kim Hammond-Kosack

Take-all (TA), caused by the fungus Gaeumannomyces tritici, is the most economically important root disease of wheat worldwide and can result in 10–50% annual yield losses. The search for resistance sources in untapped genetic material may speed up the deployment of TA genetic resistance in the field. The Watkins wheat landraces represent a valuable source of such diversity. In this study, genome wide association analysis has been done on 826 field phenotyped Watkins accessions and a stable QTL identified which spans ~10 Mb and explains 11% phenotypic of the variation. Detailed comparative genomic/transcriptomic analysis helped us to identify two differentially expressed candidate genes for TA. Based on sequencing data, diagnostic markers will be developed for the introgession of the gene(s) into UK elite commercial wheat cultivars. Moreover, this study will provide a foundational step for further cloning of a TA resistant gene(s) using a map-based approach.

Catherine E B Evans, John Innes Centre

Do NAC transcription factors regulate the timing of leaf senescence and wheat grain protein content?

Catherine E B Evans, Ruth Bryant, Juliet Coates, Philippa Borrill

High grain protein content improves both bread texture and nutritional quality of wheat. A major obstacle to improving wheat grain protein content is the negative genetic correlation between protein content and yield. The timing of leaf senescence may be linked to this trade-off: NAM-1, a NAC transcription factor, promotes earlier senescence, higher grain protein and sometimes reduced yield. To explore whether other NAC transcription factors regulate leaf senescence timing and protein content, we investigated NAC genes upregulated during leaf senescence according to RNA-seq. Results from TILLING mutant and overexpression lines suggest that some of these NAC transcription factors may influence leaf senescence timing. We are further characterising these NAC genes through field trials and identification of downstream targets. Analysing genes regulating leaf senescence and protein content could add to our understanding of the protein-yield trade-off, and open potential to improve wheat grain protein content without compromising on yield.

Nitin Uttam Kamble, John Innes Centre

Distinct biochemical mechanisms are involved in the initiation of A- and B-type starch granules during wheat grain development

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Nitin Uttam Kamble, Farrukh Makhamadjonov, Brendan Fahy,
David Seung

Starch in the wheat endosperm is vitally important as a staple carbohydrate in our diet. It is synthesised as semi-crystalline granules composed of glucose polymers. Wheat endosperms contain large A-type granules that initiate at early grain development, and small B-type granules that initiate in later grain development. We demonstrate that the plastidial α-glucan phosphorylase (PHS1), a conserved enzyme that can elongate starch polymers, plays a specialised role in initiating the B-type granules. Mutants of durum wheat deficient in PHS1 had normal A-type granules, but fewer and larger B-type granules. Starch content, grain size and grain yield per plant were not affected by the mutations. PHS1 interacts with BGC1 – a carbohydrate-binding protein essential for normal B-type granule initiation. Overall, we propose that the initiation of A- and B-type granules in wheat occur via distinct biochemical mechanisms. The implications of these discoveries to improving grain quality will be discussed.

Stephen Pearce, Rothamsted Research

Multiplexed genome editing reduces polyphenol oxidase activity in wheat grains

Forrest Wold-McGimsey, Caitlynd Krosch, Rocío Alarcón-Reverte, Karl Ravet, Andrew Katz, John Stromberger, Richard Esten Mason and Stephen Pearce.

Polyphenol oxidases (PPO) are dual activity metalloenzymes that catalyse the production of quinones and may contribute to biotic stress resistance and secondary metabolism. In wheat, PPO released from the grain aleurone layer during milling results in the discolouration of flour and dough, reducing the value of some end-use products. Paralogous clusters of POLYPHENOL OXIDASE genes are expressed in the developing grain and contribute to PPO levels but limited natural variation and small genetic distances between duplicated genes complicates the selection of low-PPO wheat varieties by recombination. We designed a CRISPR/Cas9 construct to target all POLYPHENOL OXIDASE genes and reduced grain PPO levels by more than 90% in three elite winter wheat cultivars. Our study demonstrates that multiplexed editing at late stages of variety development could complement selection for beneficial alleles by recombination in breeding programmes.

Peter Abu Jabir, University of Reading

Unraveling the biochemical and genetic basis of the perfect cookie making wheat

Peter Abu Jabir, Paola Tosi, Donal O’Sullivan, Julia Rodriguez Garcia, Sonia Miguel, Isabel Moreira de Almeida

Over half a million tonnes of soft wheat flour goes into making biscuits and other baked confectionery products in the UK each year. Despite the economic importance of soft wheat, the biochemical and genetic bases of variation in quality are poorly understood. The overall aim of this project is to conduct a genetic analysis of biscuit-making quality utilising the well-characterised NIAB 8-founder MAGIC population (which has 5 hard and 3 soft founders).

~3/8th of the MAGIC population were identified using an allele-specific PCR assay which inherited the soft alleles at the Hardness (Ha) locus. 250 MAGIC RILs carrying WT (soft) pin alleles comprise this ‘soft-MAGIC’ panel being grown over three crop years and used in all subsequent analyses. Early results show large variation among lines in cookie quality assessed via geometry and texture analyses. Grain protein content, particle size distribution and solvent retention capacity analysis are also ongoing and will be used for QTL identification.

Muhammad Ali, John Innes Centre

Iron-rich wheat: a solution for anaemia in developing countries

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Muhammad Waqas Ali, Sergio G. Lopez, Marco Catoni, Philippa Borrill

Micronutrient deficiency affects more than 2 billion people and is mainly prevalent in the poorest rural societies in developing countries. They rely on staple foods such as wheat and rice that are sustaining but often deficient in iron/zinc. Genetic biofortification through breeding offers a sustainable solution to the malnutrition problems. In this study, we screened a hundred EMS (Ethyl methane sulfonate) lines by Perls staining and selected three high iron lines with approximately three times the wild type level of iron to develop the mapping populations. Twenty plants with extremely low and high phenotype for the iron were selected from an F2 population to construct low and high bulks and subjected to bulked segregant analysis using exome capture sequencing. We are currently analysing the sequencing data which will allow us to identify the genomic regions which associate with the iron for future identification of candidate genes and introgression into breeding lines.

Stella Edwards, University of Nottingham

Photosynthetic heat tolerance in wheat's wild relatives

Stella Hubbart Edwards, Lorna McAusland, Aleyda Sierra-Gonzalez, Surbhi Grewal, Dylan Bowater, Duncan Scholefield, Stephen Ashling, Erik Murchie, Ian King, Julie King

Current global increases in temperature cause abiotic stresses in our crops with a rise of 1°C reducing grain yield by up to 6%. Photosynthesis is sensitive to this rise in temperature, which can reduce photosynthetic capacity, therefore ultimately limiting crop yields. With limited genetic variation in elite wheat lines the need to look for variation in heat tolerance is vital.

Using untapped genetic diversity from the wheat wild relatives is a way to introduce variability into wheat. Over 120 homozygous wheat wild relative introgression lines from the Nottingham BBSRC Wheat Research Centre were screened using a closed high-throughput chlorophyll fluorescence system to analyse the photosynthetic response of leaf tissue to stepwise increases in temperature.

From this screen, potential heat-tolerant introgression lines were selected for in-depth analysis of photosynthetic parameters to confirm heat tolerance. Work is ongoing to further reduce the segment size of these prospective lines.

John Ferguson, University of Essex

Chlorophyll fluorescence-based phenotyping for dissecting the genetic basis of cereal-environment interactions

John Ferguson, Zoe Wilson, Erik Murchie, Tracy Lawson,
Matteo Dell'Acqua, Johannes Kromdijk

Photosynthesis can be phenotyped rapidly via chlorophyll fluorescence (CF). Plant-environment interactions depend on photosynthetic responses. CF is therefore an important tool for screening environmental resilience. Here, two cases studies on CF approaches for screening cereal-environment interactions will be outlined:

1. A novel and low-cost platform for screening photosynthetic heat tolerance (PHT) in high-throughput was developed to survey rice populations. This platform has facilitated comparisons on the genetic architecture of PHT in African and Asian rice diversity sets and the identification of promising candidate genes for improving rice PHT.
2. Excessive light causes photooxidative damage. We have integrated a methodology for screening photoprotection kinetics into a photo-phenotyping pipeline. Through screening photoprotection responses to dynamic irradiance, we have identified substantial variation for associated traits across a maize MAGIC population. Additionally, a novel genetic mapping approach has enabled us to precisely pinpoint important photoprotection genes to target for maize improvement.

Patrick Langan, University College Dublin

Assessing Irish heritage barley in response to waterlogging: an image-based phenotyping approach

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Patrick Langan[1], Villő Bernád[1], Mortaza Khodaeiaminjan[1], Emilie Jacob[2], Joey Henchy[3], Tim Dempsey[1], Gary Gillespie[3], Jason Walsh[1,4], Eleni Mangina[4], Kevin P. McDonnel[3], Joanne Russell[5], Laurent Gutierrez[2], Robbie Waugh[5], Sónia Negrão[1]

The frequency of waterlogging is set to increase with climate change and so too will barley yield loss to waterlogging stress. The waterlogging resistance of a collection of nine Irish heritage varieties was compared to that of five commercial varieties in both field and glasshouse conditions. Working with the hypothesis that heritage barley lines may be more tolerant to waterlogging stress due to larger root systems, we sought to investigate the responses to waterlogging using high-throughput phenotyping. Field trials were assessed using unmanned aerial vehicle (UAV) mounted RGB and multispectral sensors, and showed agronomic differences between control and waterlogged conditions. Glasshouse samples were imaged daily during 14 days of waterlogging stress and seven days of recovery using three imaging sensors namely, RGB, Chlorophyll fluorescence and hyperspectral. Altogether, this work paves the way to an improved understanding of the physiology of Irish heritage cultivars and their viability as a source of waterlogging resistance.

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2. Centre de Ressources Régionales en Biologie Moléculaire, UPJV, Amiens, France
3. Crop Sciences, School of Agriculture and Food Science, UCD, Belfield, Dublin 4, Ireland
4. School of Computer Science, University College Dublin, Belfield, Dublin 4, Ireland
5. The James Hutton Institute, Dundee, United Kingdom

Arisede Chisaka, University of Reading

Addressing the challenge of combined drought and heat stress for wheat production

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In farmers' fields, drought often co-occurs with heat waves and jointly affects wheat production, but most attention has been given to the individual effects of high temperature and water limitation. Our research investigates the effects of these stresses acting together. We conducted a meta-analysis of 20 experimental studies spanning 1983–2020 to compare the effects of water limitation, high temperature, and co-occurring stress on wheat yield. Higher yield losses are observed when drought co-occurs with heat stress compared to individual stresses. The response to co-occurring stress varies with the duration of stress, crop growth stage at stress, and pot volume. We are now using experiments to develop a physiological understanding of wheat response to co-occurring stress. We are manipulating abscisic acid and cytokinin concentrations, and measuring plant water use, pollen development and yield components under individual and co-occurring stresses. The presentation will overview meta-analysis results and initial findings from our experimental work.

Jamie Orr, James Hutton Institute

A grass specific gene regulating recombination in barley

Jamie Orr, Sybille Mittmann, Dominika Lewandowska, Luke Ramsay, Robbie Waugh, and Isabelle Colas

Fine mapping in a spontaneous semi-sterile barley mutant line (BW233) led to the identification of a loss of function mutation in an E3 ubiquitin ligase which is only found in grasses – Hordeum vulgare Sticky Telomeres 1 (HvST1). Further investigation showed that loss of HvST1 function leads to incomplete assembly of the synaptonemal complex (SC) in early meiosis which regulates the number and distribution crossovers. Loss of HvST1 function in BW233 barley leads to accumulation of another key SC protein (ZYP1) and a crossover promoting protein (HEI10) near the ends of the chromosomes in early meiosis. As a result, the total amount of genetic recombination is much greater in BW233 plants, and the distribution of these crossovers is more heavily skewed to chromosome ends. These findings reveal an evolutionary divergent pathway regulating genetic recombination in cereals and presents new opportunities for the modulation of recombination in large genome cereals.

Dominique Hirsz, University of Leeds

VRNturing into the unknown: dissecting the role of *VRN2* in climate adaptation

Dominique Hirsz[1], Adam Gauley[1,2], Simon Griffiths[3], Shifeng Cheng[4], Laura Dixon[1]

Temperature and photoperiod are key environmental factors which regulate the transition from vegetative to floral growth, and when timed correctly optimise reproductive success. This is critical for high crop yields, and for cereals which experience a winter growth habit, the extended period of cold exposure called vernalisation is essential for floral transition. The cereal-specific floral repressor *VRN2* has an integral role in this pathway, yet this locus remains poorly characterised in hexaploid wheat. Our research suggests that the tandemly duplicated genes comprising the *VRN2* locus, *ZCCT1* and *ZCCT2*, show differences in gene expression patterns in varying environmental conditions. Additionally, interactions between each ZCCT protein and VRN1, alongside interactions with their promoter regions, provide new insight into the vernalisation network. Different allelic variants of *VRN1* and *VRN2* have also been analysed based on selection occurring in the Watkins collection and protein interactions testing these variants shows further specificity. Continuing to further our understanding of *VRN2* will enable the generation of more temperature-robust wheat varieties, essential to ensure high yields with a changing climate.

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4 Agricultural Genomics Institute at Shenzhen (AGIS), Chinese Academy of Agricultural Sciences (CAAS), Shenzhen, China

Ragavendran Abbai, IPK Gatersleben

Source-sink strength determines grain yield in the spike branching 'Miracle-Wheat'

Ragavendran Abbai, Guy Golan, Thorsten Schnurbusch

Introducing variations in spike architecture such as 'Miracle-Wheat' with a branching inflorescence has relevance for enhancing grain yield. However, the increase in spikelet number is not generally translated into grain yield advantage because of the trade-off among spike-branching, spikelet fertility and grain weight. Here, we investigated if such trade-offs might be a function of source-sink dynamics by using 385 RILs developed by intercrossing the spike-branching landrace TRI984 and CIRNO C2008, an elite durum cultivar. We phenotyped about 27 traits, including senescence rate under field conditions for two consecutive years. The delay in senescence increased grain set, possibly by enhanced assimilate production and re-allocation. Besides, we mapped 105 QTLs explaining these traits; importantly, favourable alleles in Chr 5A and 6B (NAM-B1) QTL hotspots are required to improve spikelet fertility and grain weight in spike-branching RILs. Taken together, achieving a balanced source-sink relationship might minimize the trade-offs affecting grain yield in miracle-wheat.

Muhammad Awais, IPK Gatersleben

Genetic control of awn roughness in barley

Muhammad Awais, Muhammad Khan, Matthias Jost, Götz Hensel,
Hélène Pidon, Robert Hoffie, Jochen Kumlehn, Twan Rutten,
Michael Melzer and Nils Stein

Wildtype barley awns are covered with upward-oriented single-celled trichomes (barbs) giving them a ‘rough’ surface, while smooth (mutant) awns lack these barbs. A major gene (Raw1) on chromosome 5H controlling barb formation has been isolated and one additional locus was detected by genome-wide association study. To characterize further this second locus, F2 mapping populations between the ‘semi-smooth’ spring barley and two very smooth mutants, were used for genetic mapping. A single locus (Raw7HS) was identified on chromosome 7H and a candidate gene for this locus was identified and validated using CRISPR-based site-directed mutagenesis. In addition, we found a strong correlation between awn barbs and the leaf epidermal hair, suggesting shared genetic control of both traits. The study describes the interaction and the role of the two genes in barb formation of different barley tissues.

Annis Richardson, University of Edinburgh

Crazy leaves and truffula trees: Unravelling auxin signalling underpinning maize architecture

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Annis Richardson[1*,2,3], Michael Prigge[4], Amber de Neve[2], Kjel Johnson[2], Aaron Sluis[2], Nicholas Morffy[5], Lucia Strader[5], Mark Estelle[4], Sarah Hake[2,3]

Crop productivity is influenced by plant architecture, which is in turn determined by the modular development of phytomers (composed of a node, organ, axillary meristem and internode). Auxin plays a key role in regulating phytomer development, however the pathway that decodes its effects is not well understood, especially in cereals. We have cloned two dominant maize mutants with opposing phenotypes; Hoja loca1(Oja) and Truffula(Trf). Oja plants often fail to produce leaves at each node. Whereas Trf plants develop extra leaves at nodes. Oja is due to a mutation in the AUX/IAA ZmIAA28, and Trf is due to a mutation in a novel, evolutionarily conserved, degron motif in the B-class Auxin Response Factor ZmARF28. Our work suggests the presence of an auxin signalling pathway that specifically regulates organ initiation, independent of phytomer formation, in cereals. This work therefore begins to shed light on the role of auxin in cereal plant development.

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(*) Current location

Miriam Schreiber, James Hutton Institute

Genomic resources for a historical collection of cultivated two-row European spring barley genotypes

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Miriam Schreiber, Ronja Wonneberger, Allison Haaning, Max Coulter, Joanne, Russell, Gary Muehlbauer, Nils Stein, Robbie Waugh

Barley genomic resources are constantly developing. Two-row barleys are of great interest due to their importance in malting and distilling. In this project we developed a data resource based on 209 two-rowed European spring barley genotypes. The population is representative of pan-European breeding progress across the years from 1830 to 2014. The dataset comprises gene expression data generated by RNA-sequencing data of six different tissues across a range of developmental stages with shallow whole genome shotgun sequencing to complement the RNA-sequencing data for variant calling. We scored 29 agronomic traits in field trials across two consecutive years across three contrasting environments in Dundee (UK), Gatersleben (Germany) and Minneapolis (USA). Here, I will give an overview of the datasets and show how and where the data can be accessed. I will also show some data use-case scenarios looking at frame shift variants, changes in gene expression and genome wide association studies.

Shradha Saraf, European Bioinformatics Institute

Ensembl Plants and the PanOryza Project

Shradha Saraf, Guy Naamati, Dmytro Chebotarov, Kapeel Chougule, Zhenyuan Lu, Sharon Wei, Yong Zhou, Bruno Contreras Moreira, Pankaj Jaiswal, Andy Jones, Ken McNally, Doreen Ware, Rod Wing, Sarah Dyer

Ensembl Plants is an integrative resource presenting genome-scale information for the analysis and visualisation of plant genomic data. Ensembl produces genome databases and can be freely accessed through our web browser, API and BioMart tools. We currently host over 125 species including many important crops including rice (Oryza sativa).

We have recently imported 15 additional Oryza sativa varieties from the MAGIC16 project, with annotations from Gramene, and these are currently displayed on the Ensembl rapid release site (**https://rapid.ensembl.org/index.html**) and will be available from our main site (with comparative analyses) later this year.

For the current rice reference (Nipponbare) there are two main annotations (RAP-DB and MSU) in use by the community which often present different models at the same locus, while other loci are only represented in one of these sets. As part of an international collaborative project (PanOryza) we are aiming to define a unified gene set for Nipponbare, combining RAP-DB, MSU and Gramene annotations. The overall aim is to create a rice pangene set, connecting gene models across the rice pangenome.

Nicola Walter, University of Nottingham

Using EMS mutagenesis to find the gametocidal gene in a wheat-*Aegilops sharonensis* introgression line

Nicola Walter, Cai-yun Yang, Duncan Scholefield, Stephen Ashling, Laura-Jayne Gardiner, Michael Wilson, Ian King, Julie King Surbhi Grewal

Wild relatives of *Triticum aestivum* are often utilised to increase wheat's genetic diversity. However, some wild relatives contain gametocidal genes. These genes ensure preferential transmission to offspring through inducing chromosomal breakages in gametes that lack them, resulting in agronomically unstable lines.

We developed gametocidal mutant lines using T4B-4S^{sh}, a wheat-*Ae. sharonensis* introgression line carrying the gametocidal gene, *Gc2*, on chromosome 4S^{sh}. Treatment of 4800 F_1 seeds with 0.3% and 0.4% ethyl methane sulfonate (EMS) resulted in 67 M_1 plants with potential loss-of-function in the *Gc2* locus. Ten progeny from each M_1 plant were genotyped to identify the 4S^{sh} segment segregation patterns. Mendelian segregation was observed in two families, confirming mutations in the gametocidal locus.

These mutant lines can be used to find the *Gc2* gene, alongside gametocidal genes in related species, and further help in targeted mutagenesis of this gene in germplasm that can then be used in breeding programmes.

Tally Wright, NIAB

Breaking the bottleneck: exploring quantitative genetics to unlock the potential of synthetic hexaploid wheat

For over a decade NIAB has been creating 'diversity-enriched' wheat with the aim of targeting the diversity bottleneck in modern cultivars, including Synthetic Hexaploid Wheat (SHW) that captures untapped introgressions from different Ae. tauschii donors. NIAB has formed a large, diverse, and powerful Nested Association Mapping (NAM) resource that consists of 3056 individuals from 54 SHW-derived BC1 F5 populations. The resource blends high statistical power with allele richness. The NAM population has been explored by growing large scale field trials (5000 plots) and we are mapping genes under exploited in UK elite backgrounds. Genomic selection is also being implemented to reduce the need to phenotype at such large scale. Due to competitive grain yield and high genetic diversity, UK-based wheat breeders have actively incorporated this novel material into their own programs. Our continued exploration of the resource will aid further future uptake and increase our understanding of NIAB's 'diversity-enriched' wheat.

Camilla Ryan, Earlham Institute

Double trouble – assembling the complex allelic diversity in outcrossed tetraploid Urochloa decumbens grass

Dr Camilla Ryan, Dr Jose De Vega

Haplotyped-resolved phased assemblies capture the allelic diversity that exists in heterozygous and polyploid species and enable the genetic analysis of complex traits and efficient breeding. Genetic maps, optical mapping and synteny have been used to resolve polyploid genomes with varying success. However, building allele-aware references still represents a significant challenge due to the difficulty of differentiating among homologues during scaffolding and limited compatible software. Here, we exploited Hi-C (high-throughput chromatin conformation capture) data, to identify long-distance interactions at the genome-wide level and assembled the genome of the outcrossed tetraploid Urochloa decumbens (2n = 4x = 36), a tropical forage Paniceae grass used to feed livestock. Our pipeline leveraged gene alleles to identify homologous unitigs, optimised scaffolding tools, and enabled manual curation of chromosomal rearrangements and misassemblies. The final phased assembly of the tetraploid U. decumbens included all 36 chromosomes and is enabling downstream analysis, like QTL mapping and GWAS analysis.

MECEA WINNER PHD

Andy Chen, John Innes Centre

Insight into wheat spike and grain development by learning from natural variation and chemically-induced mutants

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Andy (Yi) Chen, Yingqi Liu, Victoria Zeng, Ayomide Olukorede,
Junli Zhang, Adam Torrance, Nobuyoshi Watanabe,
Nikolai M. Adamski, Cristobal Uauy

Grain and spike development are two important developmental processes in wheat that can influence final grain yield. To better understand these two processes, we investigated the genetic basis of wheat subspecie and mutants that have different grain or spike morphology compared to cultivated wheat. The wheat subspecie *Triticum ispahanicum* (n = 14) have a major QTL, P2, on chromosome 6A. P2 increases the length of glume, maternal floral organs and grain. By using combination of positional-based cloning and gene editing, we discovered that T. ispahanicum has a unique 482-bp promoter deletion on the gene SHORT VEGETATIVE PHASE-A1 (SVP-A1) which is sufficient to increase glume length. ANK-15 and Nakate Gumbai have compact spike. To understand the genetic basis of spike development, we performed F2 mapping and identified a QTL on 2B. We performed RNA-seq using near-isogenic lines and identified a set of candidate genes that can influence spike development.

MECEA WINNER POST-DOCTORAL

Marek Glombik, John Innes Centre

Inheritance of divergent homoeolog expression patterns in wheat

Wheat is an allopolyploid containing three subgenomes (A, B and D), yet the regulation of these three subgenomes is still unclear. As a step towards understanding subgenome interactions we are investigating how homoeolog expression patterns vary across populations. Using biparental mapping populations we identified over 5,000 triads which show significant unbalanced homoeolog expression patterns (HEP) between F6 lines. We measured the relative distance between HEP of F6 genotypes and their parents in these 5,000 triads. In one cross a higher number of triads showed significantly more divergent HEP from only one parent rather than from both parents, whereas triads in the other cross were mostly divergent from both parents. To understand, if these trends are associated with difference in DNA sequence between the parental wheat varieties, we performed variation calling and discovered over 80,000 SNPs between parents, which we are now using to study the genetic influence on HEP.

RANK PRIZE ECR EXCELLENCE LECTURE

Amanda Cavanagh, University of Essex

Manipulating photosynthesis to boost crop productivity in a warming world

Meeting food demands for the growing global human population requires improving crop productivity, and large gains are possible through enhancing photosynthetic efficiency. But agricultural production is facing unparalleled abiotic stress from global climate change, and there is an urgent need to develop resilient crops for the extreme temperature events that now seem inevitable in the coming century. Therefore, understanding and improving photosynthetic responses to changing environmental conditions is crucial in developing high-yielding resilient crops. This talk will explore variation in the response of photosynthetic biochemistry to heat stress, and discuss the potential to exploit this for crop improvement.

RANK LECTURE

Simon Griffiths, John Innes Centre

Coordinating research to support sustainable wheat production

If you take the time to ask biologists why they chose this career they very often say something along the lines 'I wanted to make a difference'. That desire does not go away but the realities of achieving a sustainable career in science imposes changes in perspective and priority. The timelines for achieving practical impact in wheat are long and the pressure to produce publications needed to get your next job forces tough choices. For example, whether to study a relatively intractable trait which will benefit the people who are consuming wheat or the amenable trait that is a more likely bet for high impact publications but possibly less interesting as a target for future wheat varieties.

In this presentation I want to raise the profile of collaborative pre-breeding platforms within the new BBSRC wheat institute strategic programme (ISP) called Delivering Sustainable Wheat (DSW). These platforms are designed to accelerate the translation of academic research into desperately needed improvements in the sustainability of wheat production and consumption. I will use just a few examples from The Breeders Toolkit (BTK) which is the prototype for these pre-breeding platforms established in the current wheat ISP (DFW). Then describe the new platforms which are called the Demand Side Task Force (DSTF) and Gene Editing Breeders Toolkit (BTK-GE).

Finally, I will use just a few examples from my teams research of the type of pre-breeding that might go on within future BTK, DSTF, and BTK-GE. Nominations for all of these platforms are not exclusive to DSW researchers and I believe the collaborative opportunity they support can help to shift the balance of UK plant science towards that basic motivation of wanting to make a difference.

Pallavi Singh, University of Essex

Rising with the Flow: Maximizing plant resilience by exploring the connection between vascular structure and water use efficiency in cereal crops

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Grafting is the horticultural practice of fusing two plants so that they grow as one. However, this ancient and widespread agricultural practice had not been applied to the monocotyledons, which include many cereal crops. Our recent work has overturned the consensus dating back thousands of years that grasses and related species do not graft. We identified that the hypocotyl (mesocotyl in grasses) as a meristematic tissue allowing grafting. In the talk, I will outline the process of monocot grafting. I will also discuss how these findings open-up grafting as a research tool to understand plant physiology, development, and genetics in numerous cereal model systems. In particular, engineering crops to uncouple roots from shoots provides an opportunity to combat newly emerging and threatening challenges to elite cereal crops. Future research could explore the potential benefits of monocot grafting in improving crop yields and resilience to environmental stresses.

Fay Walsh, University of Leeds

Gravitropism and steeper, deeper rooting in wheat root systems

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Fay Walsh[1], Adam Binns[1], Stefan Kepinski[1]

Steeper, deeper plant root systems can improve water and nitrogen uptake from the soil and so contribute to sustainable crop production. Root growth angle is often maintained with respect to gravity, a phenomenon known as gravitropic setpoint angle (GSA). We found that seminal and lateral roots of wheat and rice maintain GSAs but had differing responses to reorientation, showing the importance of understanding species-specific gravitropic response. We have explored the role of the LAZY gene family in regulating root angle. We discovered a single-base mutation in the LAZY4 gene that induces steeper rooting in Arabidopsis. We have now identified wheat LAZY genes and characterised lazy TILLING mutants that demonstrate the potential for translating this simple, gene-editable lazy4D technology into wheat and other cereals. We will report on this work and on a new wheat DII-VENUS auxin sensor that was developed to visualise root auxin distribution during gravitropic response.

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Liam Barratt, University of York

Identifying master-regulators of abiotic stress responses in bread wheat using a network approach

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Liam J. Barratt, Zhesi He, Alison Fellgett, Lihong Wang,
Simon McQueen Mason, Ian Bancroft, Andrea Harper

With the global population expected to rise to 9 billion by 2050, a 50% increase in the yields of key crops, such as bread wheat, must be achieved within the next three decades. A major obstacle in the way of this yield increase is the changing climate, with the amount of damage caused to global wheat crops by intense heat and drought stress expected to increase drastically in the coming years. Elucidating the genes that regulate responses to heat and drought stress is integral to furthering our understanding of these processes, whilst also providing key targets for crop improvement through breeding and genetic manipulation. Weighted gene co-expression network analysis was employed to identify these stress response master-regulators, before candidate hub genes were tested to determine whether they significantly affect tolerance to these stresses.

Ji Zhou, NIAB

From images to loci: embedding AI in smartphones and drones to enable field-based yield phenotyping and mapping genetics underlying key yield components in wheat

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Jiawei Chen, Alex Swanepoel, Guohui Ding, Rob Jackson, Ji Zhou*

Recent advances in sensing technology, deep learning, and big-data analytics have opened new opportunities for plant research. Complex agronomic traits such as yield formation can now be phenotyped under field conditions using low-cost drones or smartphones. In the talk, the speaker will first introduce multi-scale plant and crop phenotyping platforms established at NIAB. Then, he will present an ongoing project supported by the One CGIAR (Seed Equal), through which an Android application (i.e. YieldQuant-Mobile, YQ-M) has been developed to measure key yield components (e.g. spike number per unit area) using smartphones. These acquired traits have empowered us to perform in-field yield prediction and the assessment of genetic gain at different sites. Moreover, using YQ-M in a large-scale screening of resource use efficiency wheat varieties, we mapped the genetics underlying target traits, demonstrating the value of low-cost and AI-powered phenotyping solutions in addressing challenging food security problems under climate changes.

POSTERS


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THE PALMER BUILDING

INTERACTIONS WITH PATHOGENIC AND BENEFICIAL ORGANISMS

Roshani Badgami, John Innes Centre

Resistance by elimination: using wheat deletion resources to identify susceptibility factors for Fusarium Head Blight

Roshani Badgami, Ben Hales, Andrew Steed, Paul Nicholson

Fusarium Head Blight (FHB) is a major disease of small grain cereals caused by Fusarium spp. It results in premature bleaching of wheat spikes and accumulation of mycotoxins in the grain, thus directly impacting crop yields and quality. Few FHB resistance loci have been incorporated into elite varieties due to association with poor agronomic performance and dependencies on environment and host genetic background. Deletion of susceptibility factors offers a novel and potentially durable strategy to achieve FHB resistance. In particular, a deletion of chromosome 4DS significantly limits fungal spread in the wheat spike. This project aims to identify the underlying susceptibility factor. Interrogation of FHB responses of a Paragon gamma-irradiated deletion population has refined an original 31.7Mbp interval to a much smaller region containing relatively few candidate genes. Identification of the 4DS susceptibility factor will provide a novel method to reduce host vulnerability to FHB.

Anisa Blower, NIAB

Exploration of NIAB's synthetic wheats as a new source of disease resistance for effective genetic control of Septoria tritici blotch disease

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Anisa Blower[1,2], Fiona Leigh[1], Rumiana Ray[2], Steve Rawsthorne[3], Kostya Kanyuka[1]

Septoria tritici blotch (STB) is an important fungal disease caused by *Zymoseptoria tritici* and results in significant yield losses of wheat. Chemical treatment for STB control accounts for 70% of Northern European fungicide use. However, high levels of genetic diversity within the pathogen population rapidly results in the loss of fungicide effectiveness and therefore developing wheat varieties with high level of STB resistance is a priority. NIAB have developed new synthetic hexaploid wheats (SHW) by crossing durum wheats with wild goat grasses (*Ae. tauschii*), as a core resource in diversifying available germplasm in the search for new genetic resistance. SHW and populations derived from them will be screened for resistance to recent UK field isolates of *Z. tritici*. Novel resistance loci will be identified, mapped and the mechanisms of resistance explored. This will provide a novel genetic armoury in the breeding of multi-isolate resistant wheat for sustainable STB management.

(1) NIAB, Cambridge, UK
(2) University of Nottingham, Nottingham, UK
(3) The Morley Agricultural Foundation, Norfolk, UK

Jack Davies, Aberystwyth University

Salinity stress alters the seed microbiome of oat and perennial ryegrass

Jack Davies, Catherine Howarth, Kerrie Farrar

The bacterial seed microbiome has key roles in promoting seedling health and growth. This study investigated the impacts on the seed microbiome of exposing mother plants to salinity stress. Oat (Avena sativa) and perennial ryegrass (Lolium perenne) were watered weekly with a 0mM, 25mM, 50mM or 100mM NaCl solution. The microbiomes of the harvested seed were profiled by 16S rDNA amplicon sequencing. Community composition showed consistency within treatment groups but there were clear differences between groups. Bacteria genera were tested for statistically significant differences in abundance between the 0mM and 100mM NaCl treatment groups. Notably, Cutrobacterium was significantly enriched under the high salinity treatment in both plant species. Changes in abundance may be driven by bacterial salinity tolerance or changes in host colonisation, such as preferential recruitment of strains that alleviate plant stress. Such strains would represent promising candidates as microbial inoculants.

Carmen Escudero-Martinez, University of Dundee

Unravelling the barley genetic control of its associated microbiota

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Escudero-Martinez C., Brown M., Brown L., Roberts D., Oburger E., Bulgarelli D., George T.S.

A prerequisite to exploiting soil microbes for sustainable crop production is the identification of the plant genes shaping microbiota composition in the rhizosphere, the interface between roots and soil. Using the cereal barley, we previously demonstrated that microbiota can be treated as an 'external quantitative trait' with the development of a novel approach using QTL mapping with microbial abundances from the barley rhizosphere. This methodology allowed the identification of barley genetic loci putatively associated with the microbes in the rhizosphere, providing a powerful tool for understanding the host genetic basis of microbial traits. One of those loci, designated the QRMC-3HS, emerges as a major determinant of microbiota composition. Building on this breakthrough, I have starting to explore the barley genetic determinants of fungal endophytes i.e., fungi that growth asymptomatically inside the plant tissues, as these may represent an untapped reservoir of beneficial functions for sustainable cereal production. Currently, I am exploring these concepts in a broad range of soils and host species, including cereals, to accelerate the development of climate smart crops in the project Horizon Europe project Root2Resilience (DOI: 10.3030/101060124).

Nida Ghori, Rothamsted Research

Genome-wide association study to map genes linked with take-all resistance in wheat using the Watkins landraces

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Nida Ghori, Gail Canning, Luzie Wingen, Dan Smith, Jitender Cheema, Feng Gong, Shifeng Cheng, Simon Griffiths, Kim Hammond-Kosack

Take-all (TA), caused by the fungus Gaeumannomyces tritici, is the most economically important root disease of wheat worldwide and can result in 10–50% annual yield losses. The search for resistance sources in untapped genetic material may speed up the deployment of TA genetic resistance in the field. The Watkins wheat landraces represent a valuable source of such diversity. In this study, genome wide association analysis has been done on 826 field phenotyped Watkins accessions and a stable QTL identified which spans ~10 Mb and explains 11% phenotypic variation. Detailed comparative genomic/transcriptomic analysis helped us to identify two differentially expressed candidate genes for TA. Based on sequencing data, diagnostic markers will be developed for the introgession of the gene(s) into UK elite commercial wheat cultivars. Moreover, this study will provide a foundational step for further cloning of a TA resistant gene(s) using a map-based approach.

Navneet Kaur, Rothamsted Research

Uncoupling the signalling network linking biotic stress and asparagine accumulation in wheat

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N. Kaur, M. Urban, K.E. Hammond-Kosack and N.G. Halford

In many plant species, asparagine plays a central role in nitrogen storage and transport. However, asparagine also acts as a precursor for acrylamide, a Class 2A carcinogen formed during cooking and processing. Asparagine accumulates in high concentrations under abiotic/biotic stresses. In wheat, fusarium head blight disease, caused by F. graminearum (Fg), reduces yield and contaminates grains with mycotoxins, e.g., DON. DON treatment in wheat increases free asparagine, glutamine, and aspartate concentration. SnRK1-type protein kinases are key regulators of plant metabolism, defence and asparagine synthesis. During infection, Fg secreted protein, OSP24, interacts with SnRK1 and accelerates its degradation. Meanwhile, wheat protein, TaFROG, competes with FgOSP24 to prevent SnRK1 degradation (Jiang et al., 2020). However, further signalling proteins/transcription factors leading to asparagine accumulation are still unknown. The current study will elucidate this network using Fg mutants, RNA-seq analysis, phosphoproteomics and proximity labelling. VIGS will then be used to validate our signalling hub.

Tom O'Hara, John Innes Centre

Identifying the wheat blast resistance gene Rmg7

Tom O'Hara, Andrew Steed, Rachel Goddard, Jesús Quiroz-Chávez, Cassandra Jensen, Kumar Gaurav, Brande B. H. Wulff, Cristobal Uauy, Beat Keller, Paul Nicholson

Wheat blast is caused by the fungal pathogen *Magnaporthe oryzae* p.v. *tritici* and was first observed in Brazil in 1985. The disease has since spread to neighbouring countries, greatly limiting South American wheat production. In addition, the devastating 2016 outbreak in Bangladesh poses a serious threat to South East Asia, notably wheat-producing giants India and China. Breeding for durable wheat blast resistance over the past 30 years has been unsuccessful, and no gene has been identified that confers resistance to *Triticum* pathotypes of *M. oryzae*. We screened the Watkins core collection of wheat using two *Triticum* isolates of *M. oryzae* carrying the *Avr-Rmg8* effector. For both datasets a significant association was observed between resistance to these isolates and a locus on chromosome 2AL.Through detailed examination of the region using the WatSeq database and IBSpy pipeline we identified a causal gene, a serine-threonine kinase. Surprisingly, it was established that this kinase has previously been identified as Pm4 which confers resistance against isolates of *Blumeria graminis f. sp. tritici*, the pathogen that causes mildew of wheat. The recognition of *Avr-Rmg8* by Pm4 was confirmed by the loss of resistance following mutagenesis of Pm4 in a resistant variety and gain of resistance by overexpression of Pm4 in a susceptible variety.

END USE QUALITY AND NUTRITION

Natasha Brock, Rothamsted Research

Re-engineering amino acid metabolism in wheat grain using CRISPR/Cas9

Natasha Brock, Swapna Nayakoti, David Withall, Vladimir Nekrasov, Mark Wilkinson, Gary Barker, Nigel G. Halford

Wheat (*Triticum aestivum*) is low in several amino acids, including threonine, methionine and lysine. Animals, including humans, are unable to synthesise lysine and so must gain it from their diet. Lysine is present in plentiful amounts in meat, but people who lead a plant-based diet, typically people in developing countries, are often lysine deficient. As people start to move away from meat dependency a sustainable source of plant-based protein will be required. Lysine is synthesised by the DAP (diaminopimelate) pathway, of which the rate limiting step is the conversion of L-aspartate semialdehyde and pyruvate into (4S)-4-hydroxy-2,3,4,5-tetrahydro-(2S)-dipicolinic acid, catalysed by the enzyme DHDPS (dihydrodipicolinate synthase). High levels of lysine are prevented from building up inside the plant due to negative feedback inhibition by lysine (Soares da Costa et al., 2018). This project will use genome editing via CRISPR/Cas9 and homology directed repair (HDR) to create wheat with high free lysine levels.

Swapna Nayakoti, Rothamsted Research

Re-engineering the amino acid metabolism in wheat grain

Swapna Nayakoti, Tash Brock, David Withall, Vladimir Nekrasov, Sarah Raffan, Nigel G. Halford

Production of animal-based protein causes a significant emission of greenhouse gases. Globally, shifting from animal to plant-based protein consumption seems to be an effective way to reduce greenhouse gas emissions. Reducing meat consumption is also an important part of achieving net zero. If that is to happen, we will need additional plant sources of lysine Wheat is one of the most important crops farmed worldwide, provides protein, fibre and vitamins to about 2.5 billion people. Humans and other monogastric animals lack the ability to synthesize certain amino acids, such as lysine, tryptophan and methionine, and lysine is present at limited levels in wheat and other cereals. Lysine is synthesized in plants from aspartate via the diaminopimelate pathway, the rate-limiting step of which is catalysed by the enzyme DHDPS (dihydrodipicolinate synthase). DHDPS is feedback-inhibited by lysine, which binds allosterically to the enzyme. This project aims to generate wheat plants with higher lysine content in the grain by altering the lysine binding site of the wheat DHDPS enzyme by cloning and PCR-based, site-directed mutagenesis. Synthesis of DHDPS inhibitors which bind the enzyme over the lysine binding site and testing them against E. coli over-expressing wild-type and mutant (lysine-insensitive) wheat DHDPS.

James Milson, John Innes Centre

Exploring heterosis of quality traits in hybrid wheat

James Milson, Marco Catoni, Nicholas Bird, Philippa Borrill

Hybridisation has been shown to greatly improve crops such as maize and rice, with heterosis being the driving force for these improvements. The production of hybrid wheat has previously been limited commercially due to high production costs. Heterosis, or hybrid vigour, is the ability of a hybrid to outperform both of its parents. This is often in terms of yield and growth, but it has also been reported in traits such as quality. To better understand how hybridisation influences quality traits in wheat we are investigating both mid- and better-parent heterosis of traits such as protein content, baking strength and baking volume. This is being tested over multiple years of hybrids produced as part of the KWS hybrid breeding program. We hope to see if quality traits are maintained between the parents and hybrids and any differences in the level of heterosis for different quality measurements.

Evans Okoli, University of Reading

Climatic impact on the nutritional characteristics of some selected inbred lines of pearl millet (Pennisetum glaucum) grown in west Africa

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About 200 million people suffer of malnutrition in West Africa (WE) and deficiencies of micronutrients is extremely widespread, largely as the result of diets based on cereal-derived food with low concentrations and reduced bioavailability of micronutrients. Pearl millet is a staple in WE and is considered a climate-resilient crop able to withstand high temperature, drought and higher atmospheric CO_2, all environmental factors predicted to increase in coming years. However, resilience is measured in terms of yield, and little is known on the effect of environment on millet's composition and nutritional quality. Our study aims to understand how climatic factors impact on the nutrients' composition and bioavailability of pearl millet. It will utilize high iron and high zinc pearl millet genotypes developed by the international crops research institute for semi-arid tropics (ICRISAT) and will determine their content and bioavailability in plants grown under controlled environment reproducing different temperature and CO_2 scenarios.

Dr Anneke Prins, Rothamsted Research

Quantifying β-glucan content in consumer food products

Janice Whonderr-Arthur, Rayan Hassan, Anneke Prins

Mixed-linkage β-glucan is a major dietary fibre in cereals that has many health benefits including reducing the risk of cancer, regulating blood sugar, and decreasing blood cholesterol. Although wheat is a relatively poor source of β-glucan, it is more widely consumed worldwide than better sources, such as barley and oat. The European Food Standards Agency recommends a daily intake of at least 3g of β-glucan to obtain health benefits. The goal of this project was to quantify the amount of β-glucan in wheat-based consumer products to determine if these products could supply the daily recommended intake. The structure of β-glucan was also analysed in these food products and compared to that observed in cereal flours to determine if processing would affect structure, and hence health-related benefits. This study was completed as part of a Nuffield student placement during summer 2022.

Luke Ramsay, James Hutton Institute

Research into barley malting quality at IBH

Luke Ramsay, Joanne Russell, Kelly Houston, Malcolm Macaulay, Pauline Smith, Robbie Waugh

The successful brewing and distilling sectors ultimately depend on the malting quality present in current barley varieties. However, there are increasing environmental pressures that potentially affect the malting quality of the crop and are that are also pushing technological changes to improve energy and water use efficiency in the malting process itself. There is therefore a need for more research into the genetic control of malting quality and its stability across environments as well as on the impact of new malting processes and end user requirements on quality parameters in the future. As part of the development of the International Barley Hub we are refocussing on the genetics of malting quality in barley. The installation of a new micro-malting facility on-site and closer links with the malting industry should allow genomic and genetic advances help ensure the future sustainability of the barley supply chain and end-user industries.

Maria Alma Sanchez, University of Reading

Bioaccessibility of provitamin A carotenoids in different corn accessions

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Maria Alma Sanchez, Paola Tosi, Donal O'Sullivan, Tonette Laude, Eureka Teresa Ocampo, Clarissa Juanico

Yellow corn exhibits tremendous natural variation for provitamin A carotenoid hence it is considered as an ideal cereal crop for provitamin A biofortification. Development of provitamin A enriched corn is promising, however bioaccessibility of this component when consumed is also an important aspect for investigation. Bioaccessibility is the amount of carotenoid coming from the food matrix that is readily accessible for human absorption. The study aimed to determine the amount of carotenoids in 23 corn accessions. Carotenoids were extracted from raw corn grits, digesta and micellar fraction. Carotenoids were analyzed in Agilent 1100 HPLC system with UV-Vis detection system controlled by Chemstation software. Detected variation for carotenoids among the corn accessions can be considered as an initial effort to initiate a breeding program to develop a carotenoid enriched corn variety. It is worthwhile to measure the availability of carotenoids in a corn variety before it can be adopted or used.

PHYSIOLOGY AND RESOURCE USE

Miles Curl, John Innes Centre

Do shared genetic pathways control drought tolerance and senescence in wheat?

Miles Curl, Simon Berry, Nick Bird, Chris Burt, Philippa Borrill

Drought is a major contributor to yield losses in wheat globally, with instances of water stress increasing due to climate change. Previous studies in crop species have shown that delaying senescence influences drought tolerance. This project hopes to identify if genetic regulation of senescence and drought in wheat is through identical transcriptional pathways to generate drought-tolerant wheat lines for use in breeding programmes. Firstly, we will build a gene network for drought responses to compare to existing networks for senescence to identify novel genes. Current drought experiments are being conducted for the senescence-related gene NAM-2. From this, we will look at the genetic variation and global environmental adaptation of both novel and previously identified senescence and drought-related transcription factors to enable the generation of new lines for further study. Utilising field trial analysis, we will explore the effects of candidate genes on senescence and drought and test our network predictions.

Anya Heathcote, NIAB

Increasing climate resilience and yield stability in wheat (*Triticum Aestivum l.*) through genetic improvement of root systems

Anya R. Heathcote, Eric S. Ober, Julia M. Davies, Lee T. Hickey, Stephen Rawsthorne

Timing and intensity of abiotic stress events are unpredictable, which has renewed interest in metrics describing the resilience of wheat yields across years and locations, and varietal differences in stress tolerance. Improvements in root system architecture are essential to optimising a plant's ability to capture resources and may enable crops to adapt to variable environments. Here, I outline my PhD proposal, where I posit that varieties with increased root biomass allocation to deep soil layers will confer greater stability under UK conditions, with little cost to yield potential. Statistical models for yield stability will be applied to multi-environment data from field trials of near-isogenic lines contrasting in root biomass and seminal root angle, and mutants exhibiting enhanced gravitropism. Research outcomes should provide breeders and growers with novel resources for the development of elite varieties suited to the rapidly changing climate.

Jake Hill, University of Nottingham

Generating wheat/*Aegilops umbellulata* introgression lines and exploring the agronomically important traits of *Aegilops umbellulata*

Jake Hill, Julie King, Ian King, Surbhi Grewal, Cai-yun Yang, Stephen Ashling, Duncan Scholefield, Stella Hubbart-Edwards

Wheat wild relatives represent an abundance of genetic diversity for the improvement of the wheat genome. This work highlights the wild relative *Aegilops umbellulata* (2n = 2x = 14, UU), the progenitor of lines developed with leaf rust resistance that helped save the American wheat crop in the 1960s. *Ae. umbellulata* has also been shown to have high protein content and heat resistance.

We discuss our approach to developing wheat/*Ae. umbellulata* introgressions utilizing the *ph1* mutant alongside addition/substitution lines. Addition/substitution lines can aid in delineating which *Ae. umbellulata* chromosome may house valuable traits. However, whole wild relative chromosomes within wheat crops can provide detrimental effects, therefore the ability to provide introgressions is vital for the improvement of wheat via wild relatives.

Finally, we show the results from a heat tolerance screen containing fifteen *Ae. umbellulata* accessions, plus addition/substitution lines and outline our future work on disease resistance and nutritional value.

Isaac Reynolds, University of York

A multi-omics approach to investigating the abiotic stress regulome of *Triticum aestivum*

Isaac Reynolds, Liam Barratt, Andrea Harper, Ian Bancroft

A worsening climate, a growing global population, and stagnating crop yields all present major challenges to meeting worldwide nutritional demand. Abiotic stresses, like drought, heat, or saline stress, reduce the yields of major crops; wheat provides up to 20% of the world's calorific intake, and so identifying sources of abiotic stress tolerance is incredibly important for preventing food insecurity and malnutrition. We aim to use transcriptomics, methylomics, and network analysis (WGCNA) to identify genes and regulatory mechanisms that underpin abiotic stress responses across a diverse panel of spring wheat landraces. We identified a number of differentially expressed genes and master regulators that may play a role in both the drought stress response and drought tolerance, and carried out further experiments on promising candidate genes to validate their importance in conveying drought-tolerant phenotypes.

Saifullah Riday, John Innes Centre

Investigating the genetic basis of the sensitivity of wheat meiosis to heat stress

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Saifullah Riday, AbdulKader Alabdullah, Cristobal Uauy

Bread wheat (*Triticum aestivum L*., 2n = 6x = 42, AABBDD) is a vital crop for global food security. Meiosis, a key biological process for sexual reproduction and fertility in plants, is one of the most sensitive stages to heat stress. Thus, increasing temperature due to climate change is predicted to impact wheat fertility and reduce grain yield. We used a novel pollen profiling method to conduct a forward genetics screen for high temperature tolerant meiotic genes in wheat using the Paragon gamma irradiation-induced deletion mutant population. The analysis revealed a strong correlation between heat stress-induced sterility and a large deletion on the long arm of chromosome 1D. In this study, we will screen Paragon lines with overlapping deletions across the large 1D deletion to refine the locus and identify candidate genes for high-temperature tolerance in wheat.

Ian Tsang, NIAB

Understanding the genetics of root hair regulation in *T. aestivum*

Ian Tsang, Pauline Thomelin, Eric Over, Jonathan Atkinson, Steve Rawsthorne, James Cockram, Fiona Leigh

Root hairs are tubular projections from individual root epidermal cells. They are critical for optimising plant nutrient and water uptake. Preliminary data indicates indirect breeder selection for wheat root hair traits. However, little is known about the genetic mechanisms and regulatory pathways governing wheat root hair development. This PhD will focus on functionally validating a network of genes controlling wheat root hair development using VIGS and TILLING, contrasting this information with the genetic architecture controlling root hair phenotypes in wheat varieties and secondary gene pools. Here, we present work investigating an EMS induced root hair-less TILLING mutant. Bulk segregant analysis and exome capture sequencing localised genetic control of this mutant to chromosome 3A. RNA-seq will be next used to investigate the expressed genes and gene expression networks in tissues of elongation and maturation zones between WT and mutant. In addition, candidates will be functionally explored using reverse genetic approaches.

Jack Walker, University of Nottingham

Use of *Thinopyrum* species to improve salt tolerance in wheat

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Jack Walker, Stella Edwards, Caiyun Yang, Duncan Schofield, Stephen Ashling, Jonathon Atkinson, Malcolm Hawkesford, Darren Wells, Ian King, Julie King, Surbhi Grewal.

Soil salinization negatively effects plant growth. Twenty percent of cultivated land and 33% of irrigated land are salt affected and degraded. To increase food security, an increase in food production on saline soils is particularly important. Bread wheat is slightly salt tolerant, however a number of its wild relatives are highly salt tolerant, particularly *Thinopyrum bessarabicum*.

In this work, 22 *Th. bessarabicum*-derived plants were grown hydroponically under different levels of salt stress in a controlled environment for four weeks. The shoot dry weight, tiller number, chlorophyll content and ion content in leaf were recorded at the end of the experiment. During high salt stress, many of the addition lines outperformed wheat in terms of shoot dry weight and low leaf sodium content.

These lines of interest will be further crossed with wheat to identify smaller Thinopyrum segments that confer salt tolerance to reduce linkage drag resulting in any negative yield penalty.

Daisy Bown, University of Southampton

The role of TaPIF3 in regulating growth of hexaploid wheat

Daisy Bown[1], Ben Sibbett[1,2], Andy Phillips[2], Lorraine E Williams[1],
Peter Hedden[2,3], Stephen G Thomas[2], Matthew J Terry[1]

The introduction of semi-dwarfing mutant alleles of *Reduced height-1* (*Rht-1)*, which encode mutants of the DELLA protein RHT-1, were key to wheat yield improvement during the Green Revolution. However, negative pleiotropic effects associated with *Rht-1* dwarfing alleles can impact their agronomic performance. With the aim of tailoring wheat growth and development more specifically, we are investigating the downstream targets of RHT-1. One potential target is the Phytochrome Interacting Factor (PIF) family of proteins, which act downstream of DELLAs in Arabidopsis. We have identified *TaPIF3*, an orthologue of Arabidopsis *PIF3*. Heterologous expression of *TaPIF3* in Arabidopsis demonstrates that *TaPIF3* can rescue the constitutively photomorphogenic phenotype of Arabidopsis quadruple loss of function *pifq* mutants. In wheat, preliminary characterisation of a *TaPIF3* mutant generated by TILLING and *TaPIF3* overexpression lines suggest TaPIF3 has a role in seedling development. TaPIF3 is therefore a promising target for manipulating wheat physiology, with further characterisation in progress.

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Adam Gauley, AFBI

Next-generation variety testing for improved cropping on European farmland

Adam Gauley, Hazel Brown, Paul Cottney, Lisa Black

InnoVar, Next-generation variety testing for improved cropping on European farmland, is a Horizon 2020 'Research and Innovation Action' project addressing 'Innovations in plant variety testing'. The project consists of 21 partners from 10 countries and is coordinated by AFBI in Northern Ireland. Using wheat as a test crop, InnoVar is devising and demonstrating improved, efficient methods of: Integrating new science into Distinctness Uniformity Stability (DUS) and Value for cultivation (VCU) plant variety testing processes, combining DUS and VCU characters, and incorporating variety information into decision-making on-farm. The project is incorporating large scale GWAS studies, advanced phenomics, with machine learning to enable assessors to allocate varieties into High Performance Low Risk (HPLR) categories based on their growth environment. This HPLR categorisation is a novel branding that will promote understanding of 'fit-for purpose' varieties and their performance by farmers and growers.

Ayushi Gupta, University of Edinburgh

Identifying gene regulatory networks and boundary specifications in maize

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A.Gupta[1], G.Chuck[2,3], A.Eveland[4], S. Hake[2,3], A.E.Richardson[1*,2,3]

The genetic specification of boundaries between distinct tissues is essential for the development of complex organs like the maize leaf. One of the most well-known genes for leaf boundary development in maize is LIGULELESS2 (LG2). lg2 mutants have defects in both vegetative and reproductive development. lg2 leaves fail to form specialized structures (ligule and auricle) at the boundary between the sheath (lower leaf region) and blade (upper leaf region). lg2 tassels (male inflorescence) have fewer branches and de-repressed bracts. This suggests LG2 is repeatedly co-opted to regulate the development of diverse organs. The molecular mechanism(s) through which LG2 regulates and influences development is still unknown. We hypothesize that the different functions of LG2 arise through tissue-specific changes in its gene regulatory network (GRN). With this view, we are using ChIPseq, RNAseq and CoIP to build the LG2 GRNs underpinning leaf and tassel development in maize.

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Katie Jeal, University of Bristol

Intercepting CLAVATA function to engineer increased ear size in wheat

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In wheat, the number of florets and grains produced are determined by the size of the ear which is determined by the shoot apical meristem (SAM). The size of the SAM is regulated by the CLAVATA signalling pathway which comprises a negative feedback loop to maintain the balance between stem cell proliferation and differentiation. CLAVATA mutants in both maize and tomato have displayed an increased yield due to an increase in the size of the stem cell pool. Wheat CLAVATA signalling components have been identified using bioinformatic approaches and TaCLV1 and TaCRN genes have been selected as for loss of function mutant generation. TaCLV1 and TaCRN loss of function mutants are currently being generated using two approaches- traditional breeding and CRISPR/Cas9 mutagenesis. The development of these CLAVATA mutants will then be investigated to determine whether disruption to CLAVATA signalling in wheat leads to an increase in yield.

Hannah Jones, University of York

Seasonality control of barley flowering: from the lab to the field

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Hannah Jones, Dr Andrea Harper, Dr Monika Spiller, Dr Hazel Bull,
Professor Seth Davis

The plant circadian clock is an internal timekeeping mechanism that integrates environmental information into a network of interlocking transcriptional feedback loops. The rhythmic outputs of the clock control a wide-ranging array of processes, including photosynthesis, resistance to biotic and abiotic stress, and floral induction. Consequently, having a circadian clock correctly matched to the photoperiod of a plant's environment confers a significant fitness advantage. Flowering is a critical agronomic trait, and its timing has long been a target for cereal breeding.

My iCASE partner, Syngenta, has introgressed clock mutations into elite winter barley cultivars, and over my PhD I have been assessing and characterising them under laboratory and field conditions. Clock mutations have historically been used to migrate barley cultivars to new latitudes, and the approaches taken in my work suggest that they could also feed into the development of cultivars with flowering times optimised to specific post-climate change agroclimatic zones.

Maximillian Jones, John Innes Centre

Identifying inhibitors of basal spikelet development using semi-spatial transcriptomics

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Maximillian RW Jones, Anna Backhaus, Nikolai Adamski, Isabel Faci, Neil McKenzie, Peter Crisp, Cristobal Uauy

Dominant alleles have played a major role in wheat domestication as recessive variation is usually masked by functionally redundant homoeologs. These are often caused by mutations in cis-regulatory elements (CREs) of transcription factors (TFs), such as PPD1 and VRN1. We propose that novel dominant variation can be generated by identifying and mutagenising CREs that negatively regulate TFs. We will test this hypothesis by attempting to manipulate early spike development. Specifically, we aim to modify basal spikelet fertility. We will select candidate TFs by comparing the transcriptomes of basal and central sections of wheat spikes across early spike development. We will also incorporate data from NILs of VRT-A2, a known regulator of basal spikelet fertility. We will then utilise ATAC-seq data, hypomethylome data, and conserved motif analyses to identify putative CREs governing those TFs. We will mutagenise these CREs in elite UK germplasm and conduct field trials on promising lines.

Roop Kamal, IPK Gatersleben

The genetic basis of apical spikelet primordia degeneration in barley

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Roop Kamal[1], Quddoos H. Muqaddasi[2], Corinna Trautewig[1], Yongyu Huang[1], Nandhakumar Shanmugaraj[1], Beata Chmielewska[3], Murukarthick Jayakodi[1], Michael Melzer[1], Henning Tschiersch[1], Nils Stein[1,4], Martin Marcher[1,5], Thorsten Schnurbusch[1,6]

The magnitude of apical spikelet primordia degeneration – also known as spikelet abortion (SA) – dictates the number of grain-bearing spikelets, thus, affecting barley grain yields. We analyzed SA and related traits in a panel of 416 six-rowed accessions to study the phenotypic associations and genetic basis underlying SA. SA was negatively correlated with final spikelet number while positively with awn length and grain morphometric traits. Our path analysis uncovered the suppressor nature of potential spikelet number. A GWAS using ~22million SNPs detected four marker trait associations (MTAs)for SA. TheChr3HMTAfor SA(PVE=18%) revealed a barley octotricopeptide repeat protein with α-helical RNA-binding (RAP) domain as a promising candidate. Natural sequence variations associated with this single copy barley RAP (HvRAP) gene showed an amino acid substitution within the RAP domain leading to enhanced SA. Similarly, HvRAPTILLING lines showed reduced photosynthetic efficiency, chloroplast defects, and decreased grain number. Our results provide a deeper understanding of SA's quantitative genetic nature and putative candidate MTAs for further in-depth cloning studies.

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India Lacey, University of Leeds

The fast and the furious: understanding speed vernalization and temperature signalling

India Lacey, Adam Gauley, Kathryn O'Connor, Laura Dixon

Winter wheat is important for the global wheat yield, however, a major challenge for research and breeding programmes is the long generation times resulting from the vernalisation requirement prior to flowering. Speed vernalisation is a protocol utilising light and temperature exposure to accelerate vernalisation satisfaction, reducing generation times without impacting traditional vernalisation response. Identifying genes involved in the speed vernalisation response is an important next step to broaden its use to more cultivars, and more winter crops. TCPs are a family of plant specific transcription factors, identified in both temperature and photoperiod responses in Arabidopsis and rice. We have identified wheat TCPs involved in the vernalisation response via QTL analysis which show temperature sensitive expression via microRNA319 regulation and interact with important floral integrators. I aim to explore how TCPs, and other candidate genes, may be involved in speed vernalisation.

Jonathan Lecoy, University of Edinburgh

Calcaroides-C as a tool for investigating 3D shape regulation

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Jonathan Lecoy, Dr Annis Richardson

Calcaroides-C (Cal-C) is a dominant barley mutant, in which the lemma develops ectopic novel sac-like and wing-like structures at the lemma-awn transition zone. Our analysis of the Cal-C phenotype shows that while Cal-C does not affect barley vegetative growth it does slow down inflorescence development. We also found a phenotypic gradient along the Cal-C inflorescence. Analysis of cell shape, also found that changes in lemma shape were preceded by changes in cell shape in the Cal-C lemma epidermis. Using a lemma-specific RNAseq analysis, we have identified an upregulation of HvKNOX8 and propose that this may underlie the Cal-C phenotype, by causing changes in the expression of abaxial patterning genes YABBY15 and KANADI1.

Katie Long, John Innes Centre

Characterising key regulators of carpel development in wheat

Katie Long, Max Jones, Isabel Faci, Anna Backhaus, Yuanrong Pei, Neil McKenzie, Nicola Trozzi, Richard Smith, Cristobal Uauy

Carpel size at and before anthesis is strongly and positively correlated with grain weight at maturity. Therefore, characterising the genetic mechanisms governing carpel development may shed insight into future breeding efforts. In my PhD, I will identify key genes involved in carpel development through transcriptomics and functional validation. Currently, I am characterising the function of *RAV* transcription factors in wheat and barley. In rice, a loss of function in *RAV* transcription factors results in an extension of the apical-basal axis in developing carpels, resulting in larger carpels at anthesis and significantly longer grains. The conservation of function of *RAVs* in the grass family remains unknown. In addition to their functional characterisation, I will further explore how *RAV* transcription factors contribute to auxin patterning in reproductive tissues. More broadly, I am also developing live imaging protocols in wheat carpels, allowing for the quantification of cell growth and division with MorphographX.

Victoria Zeng, John Innes Centre

Genetic dissection of spike development in wheat

Victoria Zeng, Andy (Yi) Chen, Nobuyoshi Watanabe, Cristobal Uauy

Wheat spike morphology is implicated in yield and several loci that influence spike length have been identified, including the COMPACTUM (*C*) and the *Q* loci. The Japanese landrace group 'Gumbai' has compact spikes and is controlled by a major QTL, C_g, on chromosome 2B. Here, we aim to identify the gene underlying C_g to attain a broader understanding of the genetic factors contributing to spike development. We generated an F_2 mapping population by crossing a Gumbai accession with Paragon. We are using whole-genome sequencing data to identify single nucleotide polymorphisms between parental lines. We will convert the SNPs into KASP markers to fine-map the C_g locus. In combination, we will perform RNA-sequencing on the developing rachis of near-isogenic lines of the C_g locus to further reduce the number of candidate genes. We hope that by identifying the gene underlying C_g, we can gain further insights into spike development.

James Brett, John Innes Centre

Fine mapping of a major QTL for high arabinoxylan fibre in bread wheat

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Simon Griffiths[1], Luzie Wingen[2], Michelle Leverington-Waite[3], Peter Shewry[4], Alison Lovegrove[5]

Increased consumption of cereal-derived dietary fibre (DF) is associated with a decreased risk of diabetes mellitus and cardiovascular disease, which are supported by approved heath claims by the EFSA and FDA. However, few consumers meet the recommended daily intake (RDI) of fibre which is 30g/day of DF. Wheat bread is a staple source of DF, supplying about 20% of DF in the UK. However, about 80% of wheat products consumed in the UK are made from white flour, which has low DF (about 4% dry wt) compared to wholegrain products (over 10% dry wt.). Despite dietary advice to consumers, the consumption of wholegrain products has decreased in the UK and increasing the DF content of the starchy endosperm of wheat (the source of white flour) is a more realistic strategy to increase DF intake.

Fibre in wheat is a heritable quantitative trait which can be targeted for improvement through conventional breeding methods. Here we report the characterisation of a robust QTL, associated with high AX, on chromosome 1BL. The parental QTL region was compared against the ‘Wheat10+’ pangenome to assess structural variation between cultivars and fine mapping carried out by developing heterogeneous inbreeding families (HIFs) and a bulked segregant approach utilising RILs from Paragon x Watkins land races crosses to reduce the size of the QTL and the number of candidate genes. This will provide understanding of the mechanism of the 1BL QTL and allow us to produce a tightly linked KASP marker at the 1BL QTL with high predictive power for AX content

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Amanda Burridge, University of Bristol

Introducing the new TaNG wheat genotyping array – the next generation in wheat genotyping

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Amanda J. Burridge, Mark O. Winfield, Alexandra M. Pzewieslik-Allen, Simon Griffiths, Luzie U. Wingen, Cong Feng, Shifeng Cheng, Keith J. Edwards, Gary L.A. Barker

The 35K Wheat Breeders' Axiom Array was launched in 2014. Since its release, global wheat breeding programmes have made major advances in introducing novel diversity into the wheat genepool from landraces, synthetics and wild relatives resulting in a new generation of wheat accessions. To navigate this novel diversity, we have developed the new '*Triticum aestivum* Next Generation' array (TaNG), designed using whole-genome re-sequencing of over 200 modern accessions and the entire Watkins landrace collection. A novel haplotype optimisation method was employed to select only highly informative SNPs, reduce marker redundancy, and has led to improvements in both physical and functional marker coverage. In addition, many markers were chosen to allow for cross-compatibility between existing genotyping platforms. As part of the public release, the new array has been tested with a global collection of wheat material. We present here the results obtained and the value of this new genotyping resource.

Delfi Dorussen, John Innes Centre

Investigating the role of DNA methylation in *Triticum aestivum* using met1 mutants

Delfi Dorussen, Samuel Burrows, James Simmonds, Cristobal Uauy, Philippa Borrill

DNA methylation is a fundamental epigenetic mark in plants, associated with transcriptional regulation, repression of transposons, and chromatin conformation. DNA methylation is catalysed by DNA methyltransferases, including MET1, which maintains CG methylation across cell division. Arabidopsis thaliana and rice met1 mutants have reduced CG methylation and altered gene expression. In wheat, CG methylation was found to correlate with a homoeologue's expression level. To further study the effect of altered DNA methylation on homoeologue expression, we have produced a population of met1 mutants in *Triticum aestivum* using TILLING lines. All double and single mutants were recovered, but not the homozygous triple mutant. The met1 mutants show developmental abnormalities, reinforcing the importance of DNA methylation for proper functioning of the wheat genome. We plan to screen for altered methylation status and use RNA-sequencing to investigate the effect on gene expression, improving our understanding of the epigenetic regulation of homoeologue expression in wheat.

Ruth Hamilton, James Hutton Institute

R-evolve: rapid evolution of wild barley

Ruth Hamilton, Malcolm Macaulay, Micha Bayer, Luke Ramsay, Robbie Waugh, Joanne Russell

Novel genetic variation has the potential to improve yield stability and enhance resilience in crops. Introducing such variation into elite germplasm is difficult due in part to problems of identifying beneficial alleles in agronomically unadapted material. In barley, very few introgressions from wild barley (Hordeum vulgare spontaneum) have been utilised in modern varieties with most exotic alleles originating from landraces. The REVOLVE project seeks to overcome some of these issues of utilising the broader wild genepool. Instead of transferring individual beneficial traits from wild into elite material, we aim to create rapidly ‘evolved’ wild barley with key domestication genes introduced from a modern elite variety. These unique partially domesticated populations will be tested both as inbred lines and as parents of F1 hybrids to screen for promising breeding material. This project acts as a proof of concept for developing more efficient breeding methods using the diversity present in undomesticated material.

Katie Hawkins, University of Leeds

Searching for bidirectional promoters in *Triticum aestivum*

Katie Hawkins, Laura Dixon

Wheat is a globally important crop with a complex hexaploid genome the regulation of which allows for a coordinated response to environmental factors such as temperature and drought. Understanding this regulation becomes increasingly important as extreme weather and temperatures become more common due to the impact of climate change. One potential aspect of this regulation is the action of bidirectional promoters, which are single promoters that regulate the expression of two genes simultaneously. For bidirectional promotion to occur the two genes must be arranged head-to-head on opposite DNA strands. I have taken a whole genome approach to bioinformatically locate bidirectionally arranged genes in *Triticum aestivum*, and confirmed that bidirectionally arranged genes are more likely to be co or anti-regulated than proximal genes. Additionally, I have used RNAseq data to predict which of these gene pairs are involved in temperature response.

Lucy Hyde, University of Bristol

Identification, characterisation, and rescue of CRISPR/Cas9 generated wheat Spo11-1 mutants

Lucy Hyde, Kim Osman, Mark Winfield, Eugenio Sanchez-Moran, James D. Higgins, Ian R. Henderson, Caroline Sparks, F. Chris H. Franklin, Keith J. Edwards

Increasing crop yields through plant breeding is time consuming and laborious, with the generation of novel combinations of alleles being limited by chromosomal linkage blocks and linkage-drag. Meiotic recombination is essential to create novel genetic variation via the reshuffling of parental alleles. The exchange of genetic information between homologous chromosomes occurs at crossover (CO) sites but CO frequency is often low and unevenly distributed. This bias creates the problem of linkage-drag in recombination 'cold' regions, where undesirable variation remains linked to useful traits. In plants, programmed meiosis-specific DNA double-strand breaks, catalysed by the SPO11 complex, initiate the recombination pathway, although only ~5% result in the formation of COs. To study the role of SPO11-1 in wheat meiosis, and as a prelude to manipulation, we used CRISPR/Cas9 to generate edits in all three SPO11-1 homoeologues of hexaploid wheat. Characterization of progeny lines shows plants deficient in all six SPO11-1 copies fail to undergo chromosome synapsis, lack COs and are sterile. In contrast, lines carrying a single copy of any one of the three wild-type homoeologues are phenotypically indistinguishable from unedited plants both in terms of vegetative growth and fertility. However, cytogenetic analysis of the edited plants suggests that homoeologues differ in their ability to generate COs and in the dynamics of synapsis. In addition, we show that the transformation of wheat mutants carrying six edited copies of SPO11-1 with the TaSPO11-1B gene, restores synapsis, CO formation, and fertility and hence opens a route to modifying recombination in this agronomically important crop.

Christopher Knight, University of Nottingham

Phenotypic assessment of stigma size across wheat germplasm

Christopher Knight, Zoe Wilson

The diversity in size and morphology of the wheat (*Triticum aestivum L.*) stigma across wheat germplasm resources is poorly known, with a larger, more-plumose stigma remaining an important target for hybrid breeding. The growing potential to phenotype large-scale populations, combined with the increased availability of marker data, offers new potential to assess and target this diversity. We have developed an image-based phenotyping protocol; and are using genome-wide association studies (GWAS), to identify potential targets to increase stigma size. We show our phenotyping protocol is robust, scalable, and able to identify a significant amount of variation across multiple collections of wheat germplasm. We are using these data to identify genetic regions of interest which, after validation, could be used as a target to improve stigma-size. The continual availability of new wheat sequence data, genetic assemblies, and deletion lines will aid swift confirmation and integration of these targets.

Lucy Mahony, Earlham Institute

Decoding the regulatory regions of wheat

Lucy Mahony, Benedict Coombes, Josh Colmer, Wilfried Haerty, Mark W. Davey, Matthew A. Hannah, Christophe Liseron-Monfils, Anthony Hall

Novel sources of genetic variation are required to increase crop production, which is critical for filling future yield gaps. Our current understanding of how genetic variation results in phenotypic changes is constrained to genes. Regulatory regions of genomes control the spatial and temporal patterns of gene expression. As such, variation in regulatory regions in wheat have the potential to be used to alter agronomically important traits by manipulating gene expression. However, they are relatively uncharacterised, with the current understanding of their function constrained to specific genes. To decode the regulatory regions of wheat, we have developed a de novo approach. Firstly, nanoCAGE data has been used to determine transcriptional start sites. This allows more accurate determination of promoter regions than the current annotation. Then identification of the local distribution of short sequences in the promoter regions allows for identification of regulatory regions upstream of genes.

Naoise McKenna, Agri-Food and Biosciences Institute

The analysis of toxigenic fungi on Irish oats

Naoise McKenna, Adam Gauley, Paul Cottney, Colin Garrett, Brett Greer, Fiona Doohan, Christopher Elliot, Lisa Black

Mycotoxins pose a serious threat to human and animal health costing the European agricultural industry over 3 billion euros over the last ten years. Climate change and agronomic factors influence the severity of Fusarium infection and mycotoxin production in crops, making it imperative to understand the underlying mechanisms to improve food security. This study focuses on the threat posed by mycotoxins produced by Fusarium fungi in oat crops (Avena sativa). A combination of analytical methods will be used for fungal and mycotoxin detection in greenhouse inoculation trials including quantitative PCR, Oxford Nanopore MinION sequencing and Liquid Chromatography Triple Quadrupole Mass Spectrometry. RNA sequencing will be used to improve our understanding of the defence mechanism of oat plants against Fusarium infection and identify genes associated with defence and mycotoxin contamination. The results will provide crucial insights into the oat plant's response to Fusarium and inform breeding efforts for Fusarium-resistant crops.

Ayomide Mary Olukorede, John Innes Centre

High throughput screening methods for *cis*-regulatory CRISPR mutants in wheat

Ayomide Olukorede, Isabel Faci, Andy Chen, Cristobal Uauy

The study of quantitative traits is confounded by functional redundancy in polyploid species such as wheat. Despite this, numerous wheat domestication traits have been identified to be caused by cis-regulatory variants. Recently, we discovered that natural variation in the *cis*-regulatory elements of SHORT VEGETATIVE PHASE genes cause the elongated grain phenotypes observed in the wheat subspecies *Triticum polonicum* and *Triticum ispahanicum*. In this work, we hypothesize that targeting cis-regulatory regions of important developmental genes in wheat can generate quantitative improvement in yield-related traits in wheat. To test this hypothesis, transgenic wheat lines containing CRISPR-Cas9 polycistronic constructs that target the cis-regulatory regions of a well-characterised transcription factor in wheat, TEOSINTE BRANCHED1 (TB1), were generated. However, screening large number of wheat transgenic lines can be laborious. Hence, this study aims to establish a high-throughput screening method to identify and characterize *cis*-regulatory mutations generated by genome editing.

Nicola Rossi, SRUC

Genetic characterization of speed breeding plasticity

Nicola Rossi, Rajiv Sharma, Ian Mackay, Wayne Powell

Speed breeding is a method of increasing the rate of genetic gain. Although empirically advanced, the underpinning biology with disruption to the circadian clock and photoperiod pathways is poorly understood. We ran a GWAS on 190 lines of the spring barley NAM population HEB-25 on time to flowering and maturity in two glasshouse environments: one of 16 hours light and 8 hours dark and the other of 22 hours light and 2 hours dark (Speed Breeding). We identified two genes as differentially associated with the traits in the two treatments, reinforcing the hypothesis that one is a suppressor of the other, decreasing its repression in Speed Breeding conditions and leading to a shorter cycle. In fact, traits' variability across environments, namely plasticity, was found to be associated with one of the two genes only, as it is upstream of the other and its expression is increased in longer dark periods.

Seamus Stack, Novogene

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Harry Jack Taylor, University of Leeds

Genetically informed machine learning models to predict T. aestivum flowering time regulation

Harry Taylor, Adam Gauley, Chetan Deva, Muhammad Jehanzaib,
Andrew Challinor, Laura Dixon

The global adaptability of bread wheat (T. aestivum) is rooted in the ability to synchronize its flowering time with favourable environmental conditions, owing largely to its exceptional genetic flexibility. To sustain UK wheat productivity under climate change projections it is imperative we quantify the genetic potential of crop ideotypes; specifically, for idealized flowering times in the predicted future climates of our target growing environments. Modelling approaches are now becoming more frequently relied upon to establish the most influential factors on performance and growth rates in key crop species.

However, few existing models incorporate genetic information to predict wheat flowering time. Three governing genetic systems underpin the flexible coordination of floral initiation, vernalization, photo period and earliness per se. Beyond these principal drivers of varietal flowering, we have identified one gene, FT3B, as having an important function in temperature dependent initiation of floral development.

Our work aims to build a predictive model of wheat growth in field conditions to identify new directions for UK regional crop breeding strategies that will produce greater flexibility in varietal flowering time of future germplasm. We include Vrn, Ppd, and FT3B as genetic predictors across multiple sites in the UK, and are presently characterising the role of TaFT3B in the vegetative and reproductive development of wheat by over expression study, tilling population analysis, and the development of NILs carrying FT3B+/-deletion in winter and spring backgrounds. These studies hope to elucidate the function of FT3Bin the flowering pathway.

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Bernice Ngina Waweru, John Innes Centre

Multi genome-based haplotype detection for disease resistance in hexaploid wheat

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Bernice Ngina Waweru, Jesus Quiroz-Chavez, Ricardo Ramírez-González, Simon Berry, Antje Rohde, Oluwaseyi Shorinola, Ryan Joynson, Burkhard Steuernagel, Cristobal Uauy

We recently developed methods for haplotype classification using chromosome-scale assemblies (Brinton et al, 2020). We further expanded this method by implementing IBSpy, a k-mer based algorithm that uses whole genome shotgun (WGS) raw reads to identify variations and define haplotypes using clustering approaches. Leveraging published pangenome assemblies improves precision and use of WGS of elite and ancestral genotypes increased the scope of diversity being examined. With this strategy, we were able to identify haplotype blocks from raw reads without the need of chromosome-scale assemblies and were able to track haplotype blocks selected by breeders. Here we elaborate on the utility of the haplotype database to identify and distinguish haplotypes with high resolution, particularly within NLR clusters that harbour disease resistance genes. Our long-term aim is to enable breeders to discover novel haplotypes and present them in a format that easily facilitates their deployment to maximise genetic gains within breeding programmes.

David Ashworth, James Hutton Institute

Does barley respond to microalgal biofertiliser?

David J. Ashworth, Naomi Villiot, Douglas McKenzie,
Davide Bulgarelli, Tom Mulholland, Kelly Houston

The use of inorganic fertilisers is essential for global food production but is also unsustainable[1]. Mining and processing damage the local environment and the climate, and P and K reserves are predicted to be depleted in the coming centuries[2, 3]. To maintain crop yields while decreasing our impact on the planet, there is a search for sustainable fertilisers. Microalgal biofertilisers and biostimulants are one source of sustainable fertiliser, which have been tested in wheat[4], barley[5] and other plants[6]. I will quantify and compare the impact of several different microalgal treatments on the growth of cv. Laureate, currently the dominant variety of barley in Scotland. To further increase sustainability, future experiments will use algae grown on nutrient rich distillery wastewater, reducing costs of treatment and creating a circular economy.

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Matteo Bozzoli, University of Bologna

The Global Durum Genomic Resource: a successful example of how genomics can be used to leverage genetic resources for increasing and characterizing the breeding value of durum varieties

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Breeding of cereal crop can be boosted by leveraging genomics tools. UNIBO and international partners assembled a golden-standard Svevo Durum wheat genome and developed a comprehensive Global Durum Genomic Resources including:

1. the Tetraploid Global Collection (TGC, 1,856 tetraploids),
2. the Global Durum Panel (GDP; 1,033 varieties worldwide), the INNOVAR panel (250 European varieties) and
3. the Tetraploid Core Collection (TCC; 350 accessions).

INNOVAR aims to revise wheat CPVO Distinctiness-Uniformity-Stability (DUS) variety registration protocols by using genomics and phenotyping techniques. The panels were phenotyped for spike fertility traits, Soil-Borne- Cereal-Mosaic-Virus (SBCMV), yellow rust response in Mediterranean environments, and DUS traits. GWAS identified peaks for grain yield components, 6 loci for yellow rust resistance and the Sbm2 locus for SBCMV resistance. Haplotype analysis identified 2288 blocks genome-wide, useful to characterize the QTL haplotypes and develop diagnostic KASP® markers. The Global Durum Genomic Resources provides unprecedented opportunities to exploit the tetraploid diversity.

Wanxin Chen, Rothamsted Research

Generation of double and triple mutant lines of sucrose: Fructan 6-fructosyltransferase (6-SFT) in hexaploid wheat may provide new breeding resources to reduce Fusarium head blight susceptibility

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Wanxin Chen, Lucy Hyde, Vinay Panwar, Wing-Sham Lee,
Kostya Kanyuka, Kim Hammond-Kosack

Fructans are important storage compounds synthesised from sucrose in many grass species including wheat with the help of three enzymes: 6-SFT, 1-SST and 1-FFT. Fructans accumulate in stems and are remobilised to spikes and grain post- anthesis. Our previous studies indicated that fructans could act as host susceptibility factors contributing to Fusarium head blight (FHB) disease severity. Homozygous Cadenza TILLING lines were identified harbouring single stop codon mutation in the three 6-SFT homoeologues on 4AL, 7AS and 7DS. After inter-crossing, double homozygous mutants 6-SFT 4AL/7DS and 7AS/7DS were identified. The generation of triple 6-SFT mutants is in progress. Simultaneously, 6-SFT and 1-SST knock-out mutants in Cadenza background were generated using genome-editing (GE). Phenotyping of all TILLING and GE fructan biosynthesis pathway mutants for FHB resistance is in progress. These mutants will be explored as a new resource for future breeding strategies to increase resilience against fungal diseases.

Jed Clark, University of Leeds

Wheat contra weed: Identifying wheat germplasm for enhanced competition against black-grass

Jed Clark, Tom Bennett, Lynn Tatnell

New approaches of IWM are required to combat black-grass in Winter Wheat. Competitive cultivars have been highlighted as a way of naturally suppressing black-grass. Identifying competitive cultivars is time staking, there is little evidence of above ground crop-black-grass competition and less is known on their below-ground interactions. Focussing below-ground, does crop root growth determine its competitive ability against black-grass? We hypothesise black-grass gains a competitive advantage over wheat due to:

1. an increased investment in the root system
2. faster growth in winter conditions
3. prolonged period during the winter to grow roots.

These three factors allow black-grass to dominate below-ground space and resources by the spring. By comparing WW varieties both elite and landrace as well as varieties of winter barley we see different competitive abilities against black-grass in both lab and in container trials. This provides hope for competitive cultivar use in weed suppression.

Ritesh Gosh, Imperial College

Mechanostimulation: a promising strategy for sustainable agriculture

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Ritesh Ghosh, Naomi Nakayama

Environmental stresses cause a threat to agriculture as it reduces global crop production by half. Besides, as agricultural modernization progresses, we are now facing serious ecological consequences, such as the destruction of farmlands due to the excess deposition of chemicals (fertilizers and plant protection products). We need more sustainable approaches to improve food security. Interestingly, repetitive exposure to mechanical cues, such as touching, bending, and vibration, can bolster the structural strength and basal defence responses of plants. It suggests that mechanostimulation methods are promising for next-generation agricultural improvement. By gaining a mechanistic understanding of the processes, we can optimize the mechano-priming protocol for a broad range of crops. We are investigating the dynamics by which barley plants respond to different doses of mechanical stimulation, quantifying the changes in the plant architecture and cross-stress tolerance (e.g., lodging and drought).

Michael Hammond-Kosack, Rothamsted Research

Introgression of Triticum monococcum into hexaploid wheat: a novel germplasm resource for trait improvement

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Michael Hammond-Kosack, Kostya Kanyuka, Kim Hammond-Kosack

The diploid, grass relative Triticum monococcum harbours an unusually large number of desirable traits for introgression into hexaploid wheat, including broad spectrum resistance to many pathogens and various crop architecture traits. Three T. monococcum accessions were successfully bred into Paragon, using T. durum as a bridging species and ~1000 individual near homozygous lines generated. Traits characterised under glasshouse conditions included ear architecture, grain number, thousand grain weight (TGW) and grain colour. 46 introgressed lines (~4%) had a higher TGW and seed numbers than Paragon. When field trialled in 2020, six plants with high yellow rust resistance were identified and many others showing the Disease Lesion Mimic (DLM) phenotype, which promises broad spectrum resistance. In 2023, the field trial will be drilled in early March. All interested parties are invited to visit/assess/score the trial and become part of the new network NIFTYR – Network for Introgression Field Trials for Yield and Resistance.

Kelly Houston, James Hutton Institute

Functional mutations of HvHKT1;5 influence yield relted traits and compostion of barley grain

Kelly Houston, Pauline Smith, Christoph Dockter, Pai Pedas,
Robbie Waugh

Soil salinity, most prominently the product of NaCl accumulation induced by a combination of natural and anthropogenic events that include irrigation and climate change, is a major factor affecting agricultural production worldwide. We identified and characterised a gene, HvHKT1;5 as being responsible for the variation in sodium accumulation in contemporary barley cultivars. Furthermore, we identified the functional SNP underlying this variation (Houston et al 2020). Building on our hypothesis that accumulation of sodium (Na) could be beneficial on low potassium (K) soils we have grown mutant lines from the FIND-IT Planet library (Knudsen et al. 22) which have alternative alleles of this gene on different combinations of Na and K. We quantified a range of yield related traits and analysed the composition of the grain ionome. Here we will discuss the results, and our plans for field scale trials soon.

Stephanie Swarbreck, NIAB

Improving tef production through better root systems

Fasil Asmare, Alek Ligeza, Anya Heathcote, Kassahun Admkie, Kekebew Assefa, Ji Zhou, Stéphanie Swarbreck

Tef (*Eragrostis tef (Zucc.) Trotter*) is an orphan cereal crop from East Africa, that is widely cultivated by small-holder farmers in Ethiopia as it is grown on 30% of the total cereals area cultivated. Tef plants are highly susceptible to lodging, which can lead to an overall yield reduction of 17% or more. We propose that selecting tef genotypes with thicker roots and a wider angle between seminal roots would provide a stronger anchorage and would significantly improve tef yields in Ethiopia. We have screened a tef mutant population for root system architecture and developed a bespoke high-throughput imaging system. We identified interesting lines with either very wide or very narrow angle. We have also analysed the root architecture of popular tef varieties to link these data with field level data of lodging and identified differences amongst varieties adapted to wet vs dry area.